

FIGURE 1A

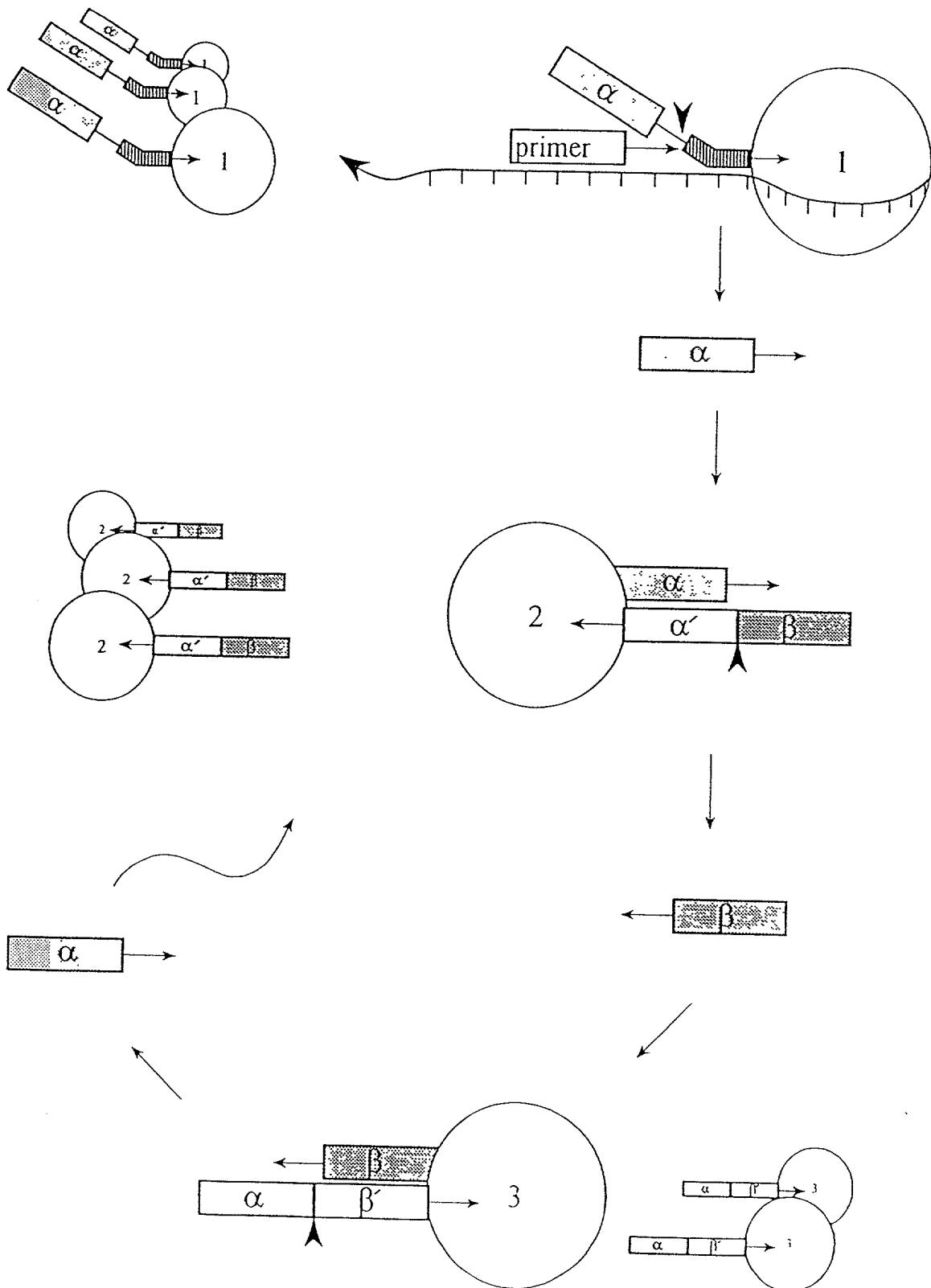
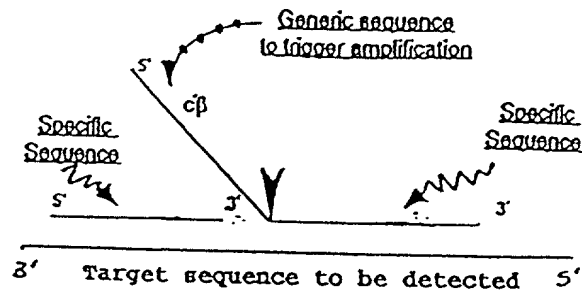
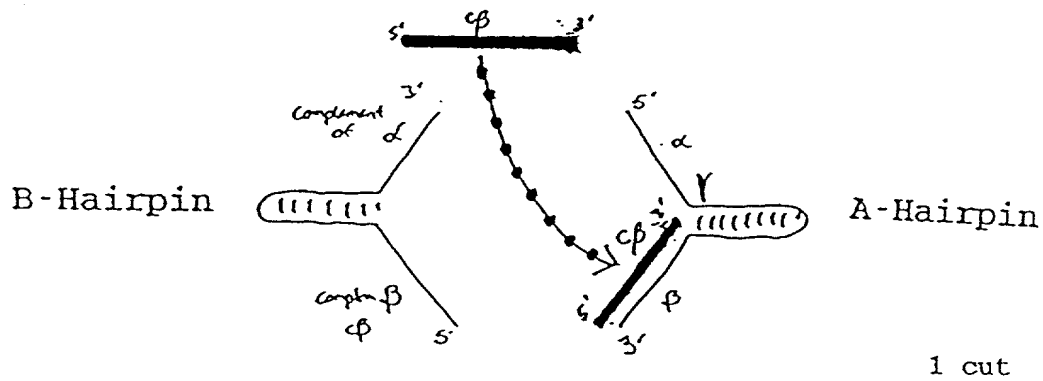


FIGURE 1B

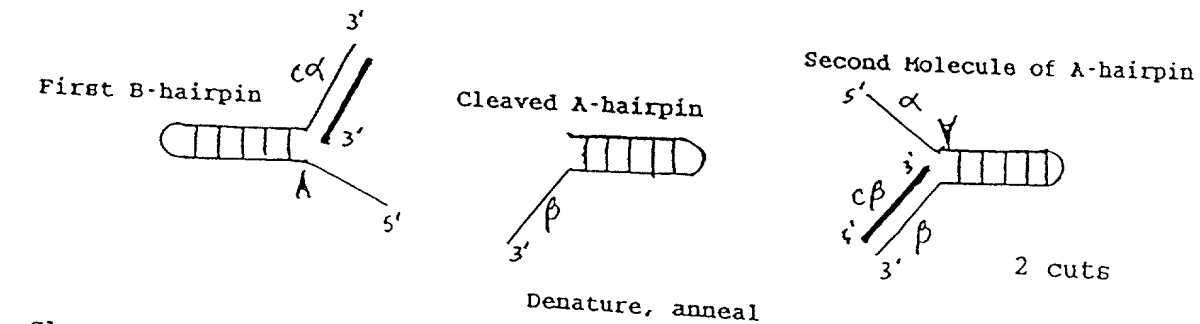
PART ONE: TRIGGER REACTION



PART TWO: DETECTION REACTION



Denature, anneal



Denature, anneal

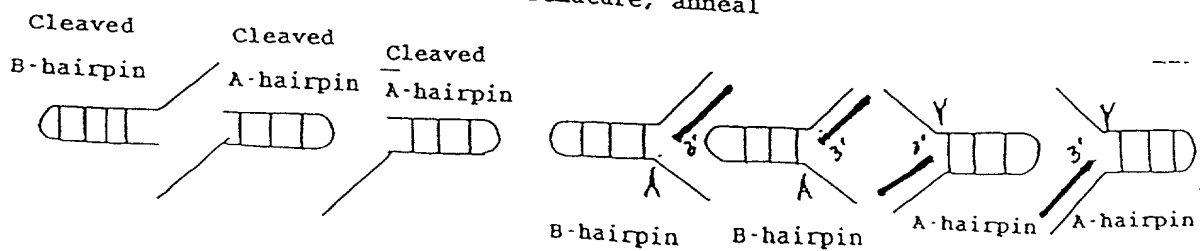


FIGURE 2 (cont'd)

MAJORITY (SEQ ID NO:7)	TCCAGGCCCCACATCGGAXGACCTGAXGCTCTCCTGGAGGCTXTCGCCAGGTGGCCACCGACCTGCCCGCTGGA	
DNAPTAA (SEQ ID NO:1)	...T.....C..T...A.....C..GG..A.....	764
DNAPTAL (SEQ ID NO:2)	...GGG...G.C...GCC..T..C..A...T.....A...T.....	761
DNAPTTH (SEQ ID NO:3)	..A.....C.....A.....C.G.....T.....C.....G.....C.....	770
MAJORITY	GCTGGACTTCGCCCAAGXGGGGGAGCCCCGACCGCGAGGGGCTTAGGGCCCTTCTCGAGAGGCTGGAGTTT	
DNAPTAAAA.....A.....A.....A.....T.....	834
DNAPTALGG.G.C.C..CACA...A...T.....T..GC...T...T...C..T.....	831
DNAPTTHC.....C..G.....G.....G.....C.....C.....	840
MAJORITY	GGCAGCCCTCCTCCAGGAGTTGGGGCTTCTGGAGGGGGCCCAAGGCCCTGGAGGAGGCCCGCCCGCCG	
DNAPTAAT.....T.....AA.....	904
DNAPTAL	..A.....G.....G.....G...G...GCCA.....T..	901
DNAPTTHG.....C.....GCCG.....	910
MAJORITY	CGCAAGGGGCCCTTCGTGGCCCTTGTCCCTTCCCGCCCGCCGAGCCCATGTGGCGCCGAGCCTTCTGCCCGCTGCC	
DNAPTAAT.....G.....AAG.....T.....	974
DNAPTALT..T.....TC.T.....T.....	971
DNAPTTHC.....C.....G.....G.....AAA.....	980
MAJORITY	CCCCGCCAGGGGAGGGGGCGGGTCCACCGGGGCGACGAGCCCTTTAXGGGCCCTXAGCGACCTXAAGCGAGCTG	
DNAPTAAG.....C.....C..G..T.A..AA.C...C.....G.....C..	1044
DNAPTAL	T.GG...GT.....G..CC...T.....A.....C.....G.....G.....T.....G.....	1041
DNAPTTHTG.....C.....G.....G.....GGC...G..A.A.....C.....C.....	1050

5

FIGURE 2 (cont'd)

MAJORITY (SEQ ID NO:7)	GGAGATCGCGCGCGCTCGAGGAGGAGGTCTTCCGGCTGGCGCGGCCACCCCTTCAACCTCAACTCCCGGGGAC	
DNAPTAO (SEQ ID NO:1)GC.....CC.....	1464
DNAPTFL (SEQ ID NO:2)G.G.....AG..G.....	1461
DNAPTTH (SEQ ID NO:3)T.....T.....G.....	1472
MAJORITY	CAGCTGGAAAGCGTGCCTTTGACGAGCTXGGGGCTTCGGCGCATCGGCAAGAGCGGAGACXGGCAAGC	
DNAPTAOG.....C.....A.....	1534
DNAPTFLGC.....G.C..G..T.....	1531
DNAPTTHTA.....T.G..G.....C.A.....	1540
MAJORITY	GCCTCCACCGCGCGCGCTGCTGGAGGCGCTXCGXGAGGCGCCACCCCATCGTGGAGAGAGATCCTGCAGTA	
DNAPTAOC.....C.....C.....	1604
DNAPTFLT.....G..A.....GCGC.....	1601
DNAPTTHG.....A..G.....C.....C..C..	1610
MAJORITY	CGCGGAGCTCACCAAGCTCAAGAACACCTACATXGACCGCGCTGCCXGXCTCGTCCACCCCGAGGACCGGGC	
DNAPTAOG.....G.....T.....G.A.....A.....	1617
DNAPTFLA.....A.....G.C..G.....A..C.....	1614
DNAPTTHG.C.....C..AAG.....G.....	1680
MAJORITY	CGCCCTCCACACCGCGCTTCAACCAGACGGCGCCACGGCGCAGGCTTAGTAGCTCCGACCCCAACCTGC	
DNAPTAOA.....A.....T.....C..	1744
DNAPTFLG.....C.....TCG.....	1741
DNAPTTHG.....G.....	1750

FIGURE 2 (cont'd)

MAJORITY (SEQ ID NO:7)	AGAACATCCCGCTCCGCCACCCXCTGGCCCAAGAGGATCCGCCCGGCCCTTCGTGCCCGAGGACGGCTGGCT	
DNAPTAA (SEQ ID NO:1)G..T..G.....A..C.....C...C..	1814
DNAPTTL (SEQ ID NO:2)G.....T.....C..C.....A.....C.....C.....	1811
DNAPTTH (SEQ ID NO:3)CT.....C.....C.....C.....C.....C.....	1812
MAJORITY	GTGGTGGCCCTGGACTATAGCCAGATAGAGCTCCGGTCCGTGGCCGACCTCTCCGGGGAGGAGAACCTG	
DNAPTAA	A.....T..T.....G.....A.....G.....C.....C.....	1884
DNAPTTL	.C.....T..T.....G.....T.....T.....C.....C.....	1881
DNAPTTHC.....C.....C.....C.....C.....A.....C.....	1890
MAJORITY	ATCCGGCTCTCCAGAGGGAGGACATCCACACCCAGACCCGACCTGGATGTTCCGGCTCCCGCCCGG	
DNAPTAAC.....C.....GG.....C.....G.....G.....	1954
DNAPTTLT.....T.....C.....C.....C.....C.....C.....	1951
DNAPTTH	A.....A.....A.....A.....A.....A.....A.....	1960
MAJORITY	AGCCCGTGGACCCCTGATCGCCCGGGGGCCCAAGACCATCAACTTCGGGCTCCTGTACGGCATGTCCGG	
DNAPTAAA..GG..A.....T.....C.....C.....C.....C.....	2021
DNAPTTLA..GG..A.....T.....C.....C.....C.....C.....	2021
DNAPTTHA..GG..A.....T.....C.....C.....C.....C.....	2030
MAJORITY	CCACCGGCTCTCCAGGAGCTTCCCATCCCGTACCGAGGAGGGGGTGGCGCTTCATTGAGCGGCTACTTCCAG	
DNAPTAAA.....A.....T.....C.....C.....C.....C.....	2094
DNAPTTLGG.....T.....T.....C.....C.....C.....C.....	2091
DNAPTTH	...TA..G.....C.....C.....C.....C.....C.....C.....	A 2100

8

FIGURE 2 (cont'd)

MAJORITY (SEQ ID NO:7)	AGCTTCCCCAAAGCTGGGGCCCTGGATTGAGAAAGACCCCTGGAGGAGGGGAGGGGGGCTACCTGGAGA	
DNAPTAO (SEQ ID NO:1)	2164
DNAPTL (SEQ ID NO:2)	2161
DNAPTH (SEQ ID NO:3)	2177
MAJORITY	CCCTCTTCCGGCCGGGGCTAGCTGCCCCGACCTCAACCCCGGGTGAAGAGCGTGGGGGAGCGCGCGGA	
DNAPTAO	2234
DNAPTL	2231
DNAPTH	2240
MAJORITY	GGCGATGGCCCTTCAACATGCCCGTCCAGGGCACCGCCCGGACCTCATGAAGCTGGCCCATGGTGAAGCTC	
DNAPTAO	2304
DNAPTL	2301
DNAPTH	2310
MAJORITY	TTCCCCCGGCTXCAGGAAATCGGGGGCAGGATGCTCCTXCAGGTCCACGACGAGCTGCTCCTCGAGGGCC	
DNAPTAO	2371
DNAPTL	2371
DNAPTH	2380
MAJORITY	CCAAAGAGCGGGCGGAGGCGGTGGCCCGCTTGGCCCAAGGAGGTGATGGAGGGGGTCTATCCCGCTGGCGGT	
DNAPTAO	2444
DNAPTL	2441
DNAPTH	2450

FIGURE 2 (cont'd)

MAJORITY	(SEQ ID NO:7)	GGCCCTGGAGGTGGAGGTGGGGATGGGGGAGGACTGGCTCTCCGCCAAGGAGTAG	
DNAPTAA	(SEQ ID NO:1)A.....	2499
DNAPTLL	(SEQ ID NO:2)CC.....	2496
DNAPTTH	(SEQ ID NO:3)T.....GT...	2505

FIGURE 3

MAJORITY (SEQ ID NO:8)	MXAMLPLFEPKGRVLLVDGHHLAYRTFFALKGLTTSRGEPUQAVYGFAKSLLKALKEDG·DAVXVVVFDK	
TAQ PRO (SEQ ID NO:4)	RC.....H.....	9
TL PRO (SEQ ID NO:5)V.V.....	
TTH PRO (SEQ ID NO:6)	E.....YK..F.....	70
MAJORITY	APSFREAYEAYKAGRPTPEDFPROLALIKELVDLLGLXRLEVPQYEADDVLATLAKKAEKEGYEVRL	
TAQ PRO	GG.....A.....S.....	139
TL PROV.....F.....R.....	138
TTH PROFT.....	140
MAJORITY	TADRDLYQLLSDRIAVLHPGYLITPAWLWEKYGLRPEQWVDYRALXGDPDSNLPQVKGICEKTAXKLLX	
TAQ PRO	K.....H.....D..A.....T..E.....R...E 209	
TL PROE...I.....Y.....A.....I.....QR..R 208	
TTH PROV...V.....H.....E.....F...V.....L...K 210	
MAJORITY	EWGSLNLLKNLDRVKP·XXREKIXAHMEDLXLSXXLSXVRTDLPLEVDFAXRREPDRGLRAFLERLEF	
TAQ PROA.....L...Al...L...D...K..WD.AK.....K.....R.....	278
TL PROFOH..Q...SL...LO.G..A.A..RK..O.H.....GR..T.NL.....	277
TTH PROENV.....K..L...R..LE..R.....L.OG.....	280
MAJORITY	GSLLHEFGLLXPKALEEAPWPPPEGAFVGFVLSRPEPMWAEILLALAAARXGRVHRAXDPLXGLRDLKEV	
TAQ PROS.....K.....D.....G.....PE.YKA.....A 348	
TL PROG...A.....L..SF.....G.WE..L...O...R.....G. 347	
TTH PROA.AP.....K.....C.D.....A...A..K..... 350	

FIGURE 3 (cont'd)

MAJORITY (SEQ ID NO:8)	RGLLAKOLAVLALREGLDLXPGDDPMLLAYLLDPSNTTPEGVARRYGGEWTEADAGERALLSERLFXNLXX	
TAQ PRO (SEQ ID NO:4)	S.....G.P.....E.....A.....A.....WG	486
TRL PRO (SEQ ID NO:5)	I.....F.E.....A.....A.....QT.KE	487
TTH PRO (SEQ ID NO:6)	S.....V.....AH.....HR..LK	490
MAJORITY	RLEGEERLLWLYXEVEKPLSRVLAHMEATGVRLDVAYLOALSLEVAEEI RRLEEEVFRLAGHPFNLNSRD	
TAQ PRO	R...R...A.....R.....A.....A.....	488
TRL PRO	K.....E.....R.....EA.V.O.....	487
TTH PRO	K.....H.....L.....	490
MAJORITY	QLERVLFDELGLPAIGKTEKTGKRSTSAAVLEALREAHPIVEKILQYRELTCLKNTYIDPLPXLVHPRTG	
TAQ PROS.....S.....D.I.....	558
TRL PRODR.....A.....K..	557
TTH PRO	R...L...Q.....H.....V.....S.....	560
MAJORITY	RLHTRFNOTATATGRLSSSDPNLONI PVRTPLGQRI RRAFFVAEEGWXLVALDYSOIELRVLAHLSCDENL	
TAQ PROL.....I.....L.....	628
TRL PROV.....V.....	627
TTH PROA.....A.....	630
MAJORITY	IRVFQEGRDIHTQTASWHF GVPPEAVDPLMRRAAKTI NFGVLYGMSAHRLSOELAI PYEEAVAFIERYFO	
TAQ PRO	E.....R.....Q.....	698
TRL PRO	S...G.....G...S.....	697
TTH PRO	K.....V.....	700

FIGURE 3 (cont'd)

MAJORITY (SEQ ID NO:8)	SFPKVRWIEKTL ECGRRRGYVETLFGRRRYVPDLNARVKS VREAAERMAFNMPVOGTAADLMKLAHVKL	
TAQ PRQ (SEQ ID NO:4)E.....	70
TRL PRQ (SEQ ID NO:5)	.Y.....G.....	767
TTH PRQ (SEQ ID NO:6)K.....	770
MAJORITY	F PRLXEMGARM LQVHDELVL EAPKXRAEXVAALAKEVMEGVYPLAVPLEVEVGXGEDWLSAKEX	
TAQ PRQE.....A..R.....	833
TRL PRQQ.L.....D..R.....W..Q.....L.....	831
TTH PRQR.....L.....QA...E.....A..KA.....M.....G	835

Genes for Wild-Type and Pol(-) DNAPTaq

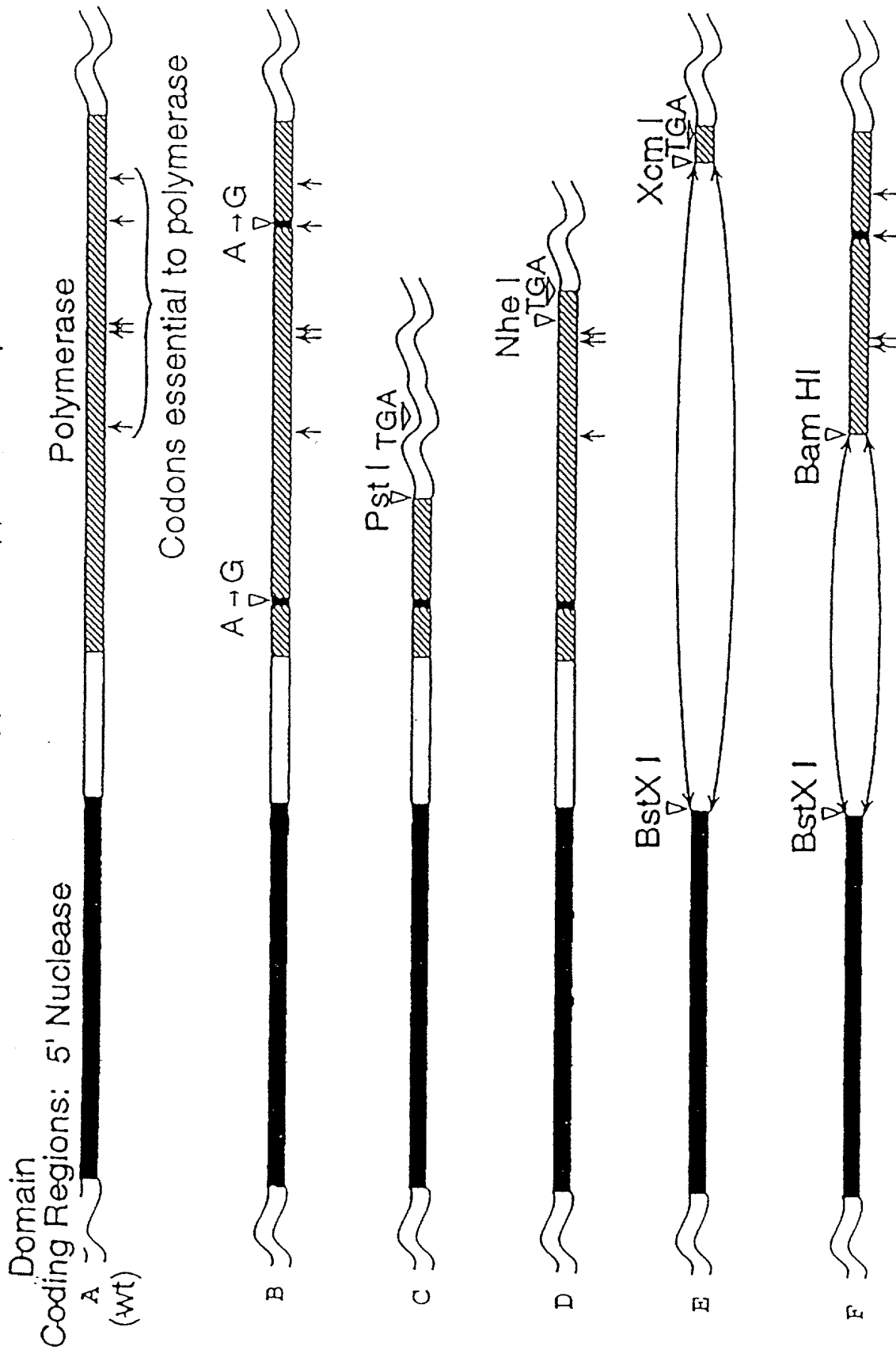


FIGURE 5

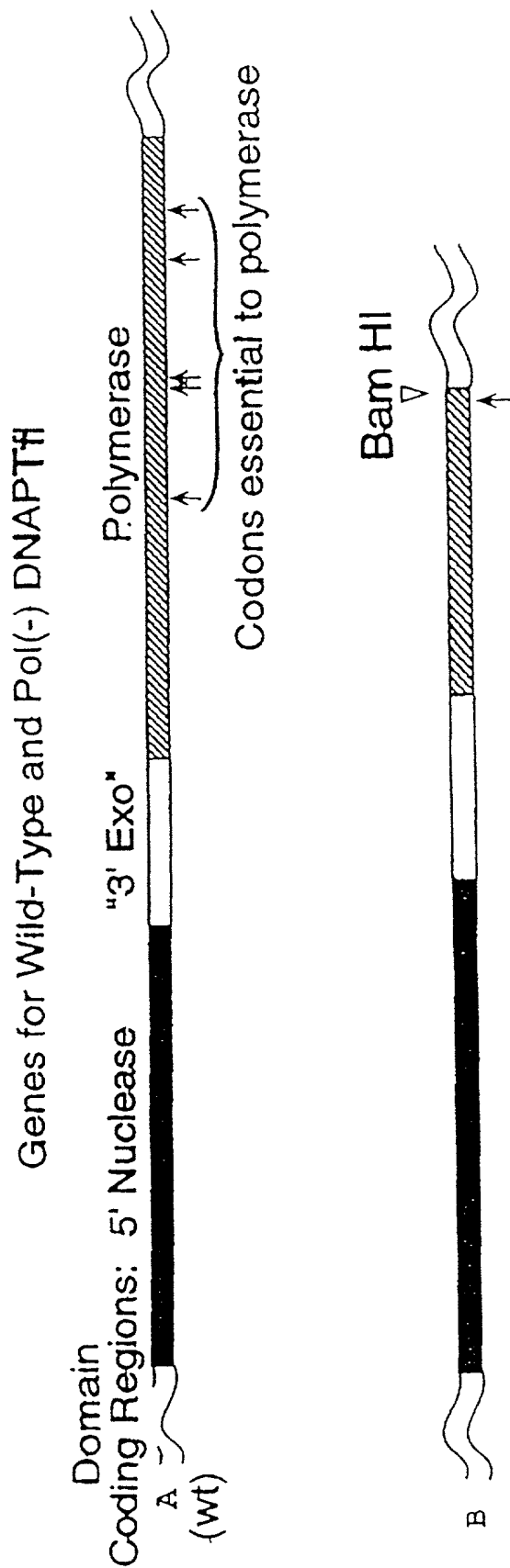
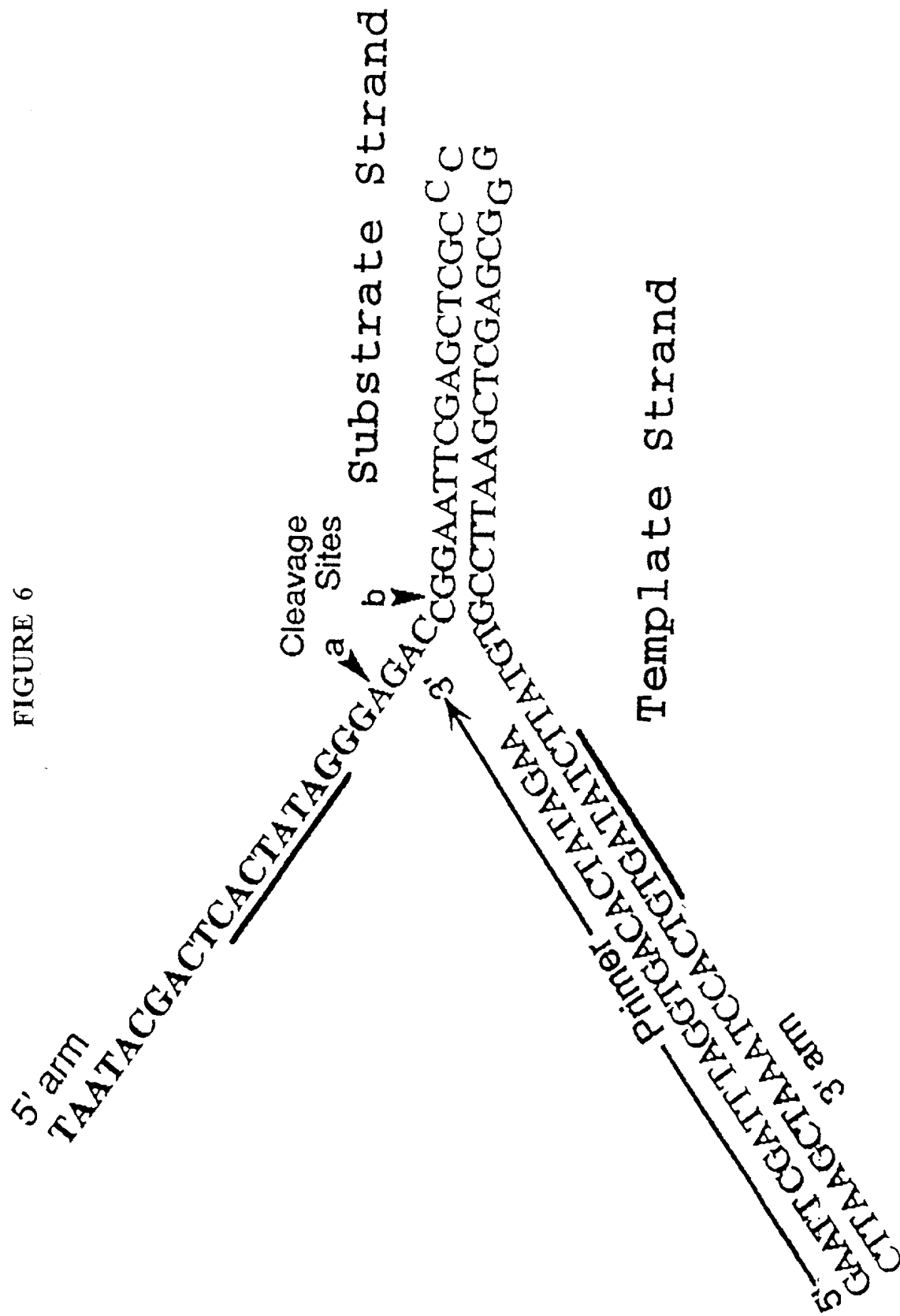


FIGURE 6



100433 03400

FIGURE 7



FIGURE 8

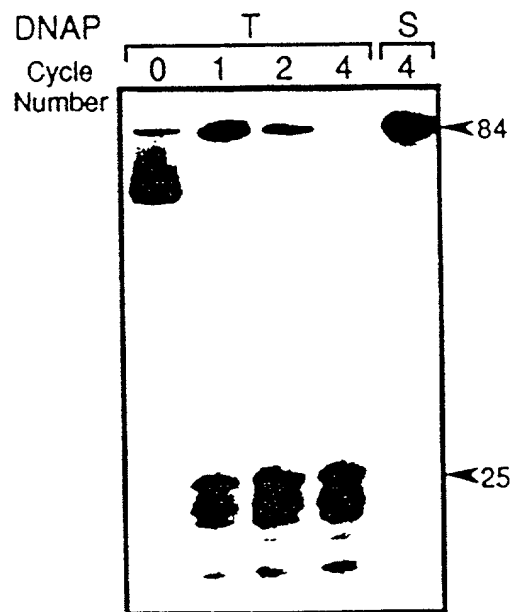


FIGURE 9

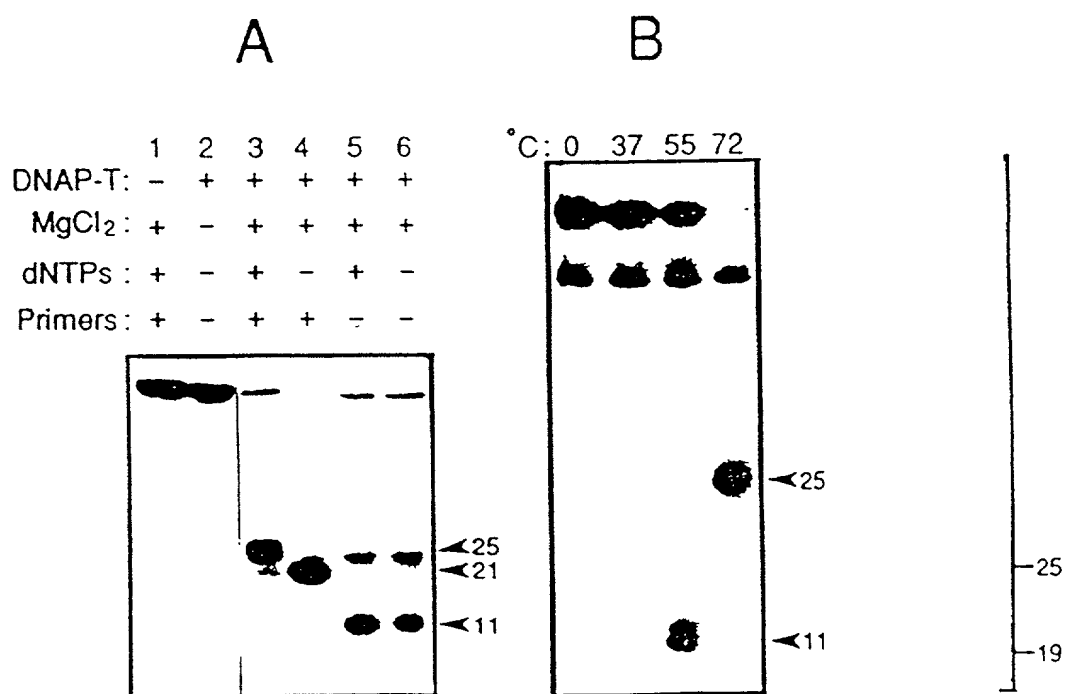


FIGURE 10

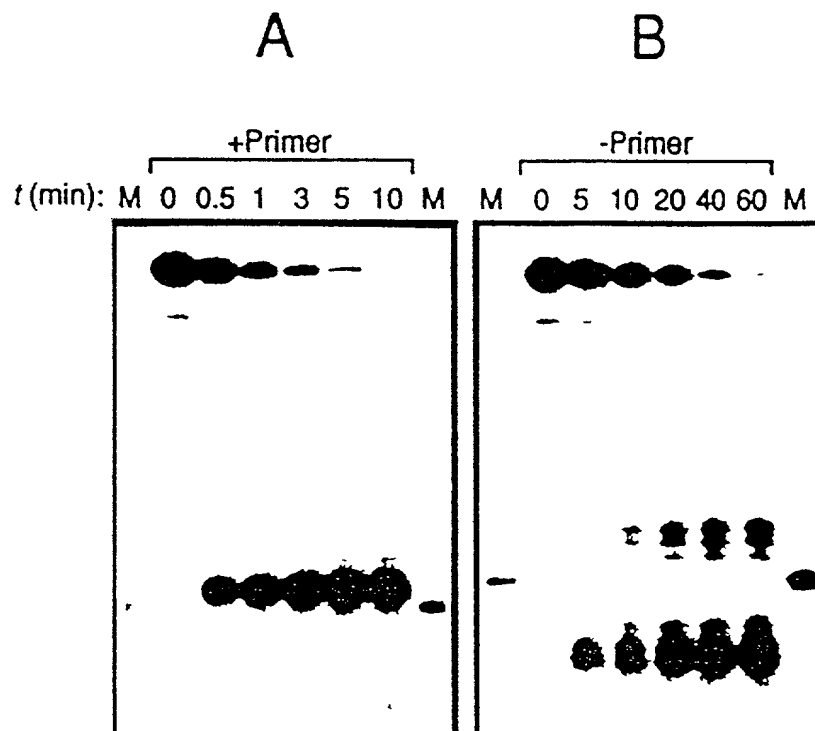


FIGURE 13

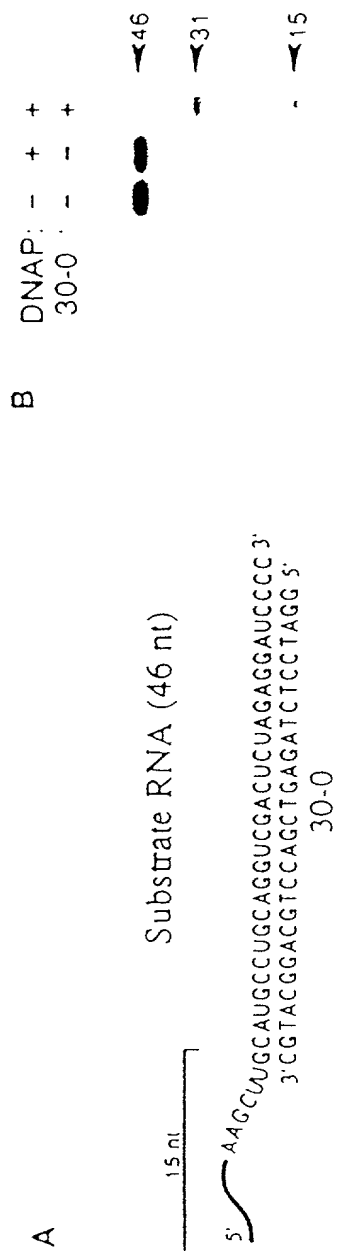


FIGURE 14

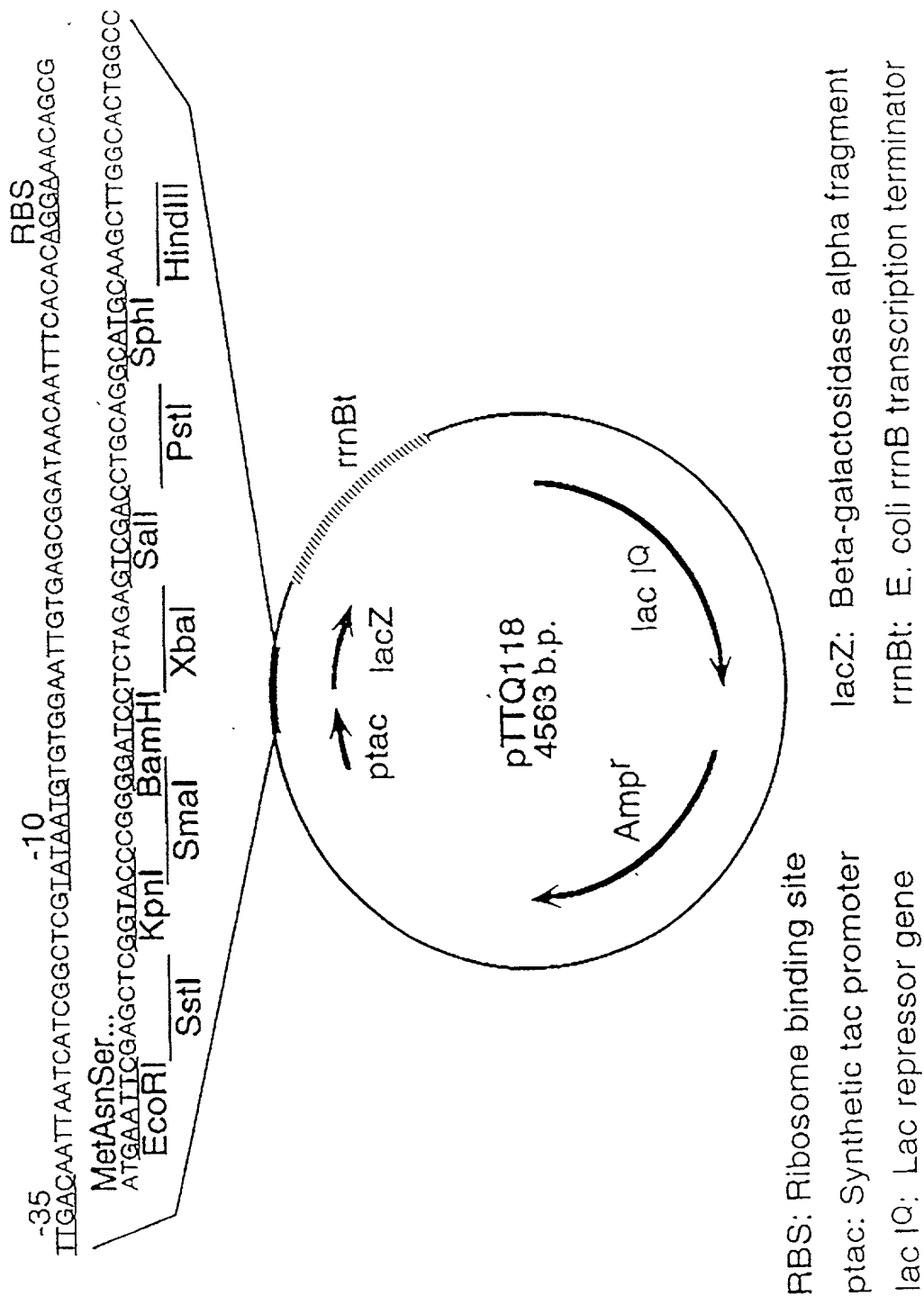
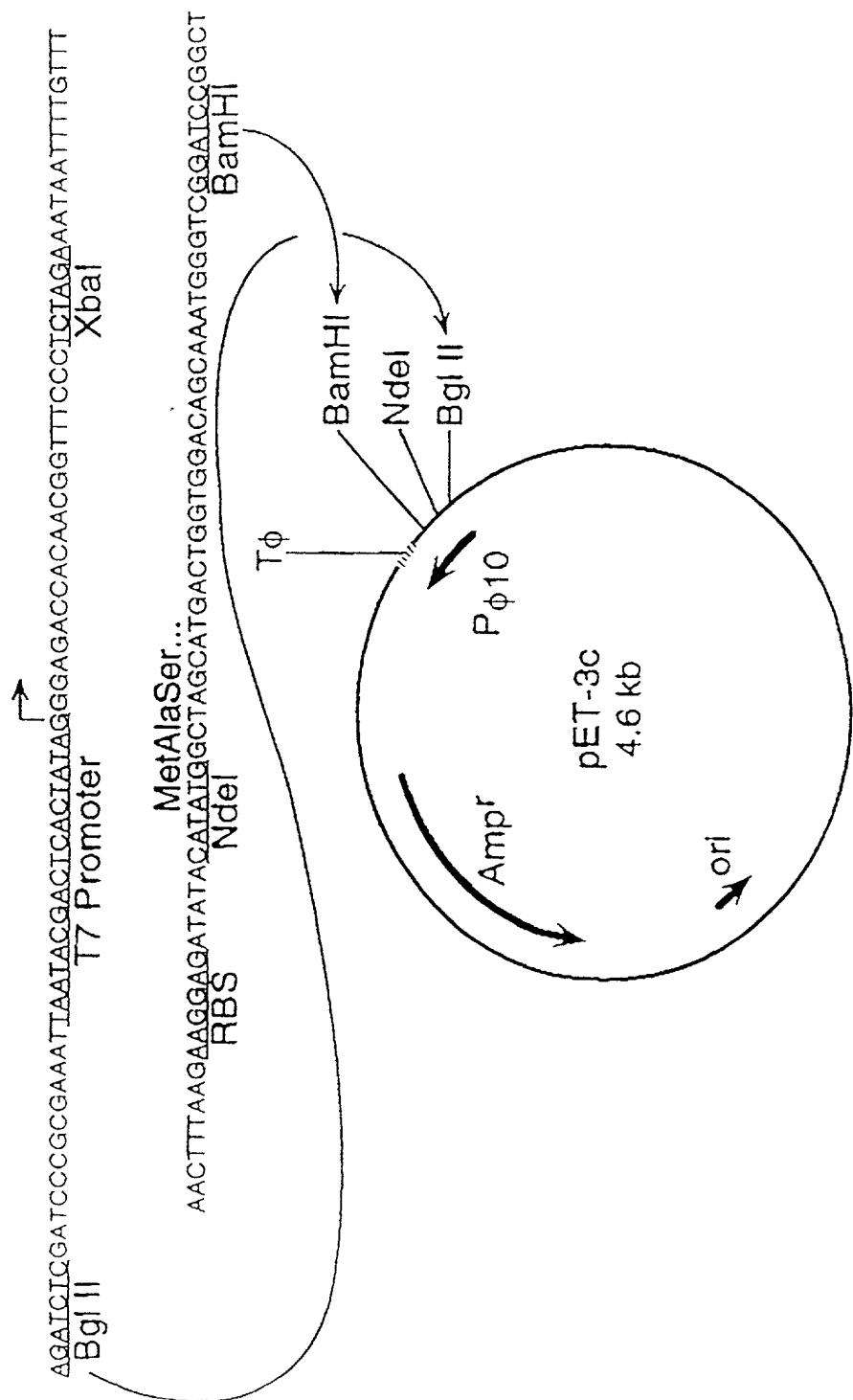


FIGURE 15



P_{φ10}: Bacteriophage T7 φ10 promoter
 T_φ: T7 φ Terminator
 RBS: Ribosome binding site

FIGURE 16

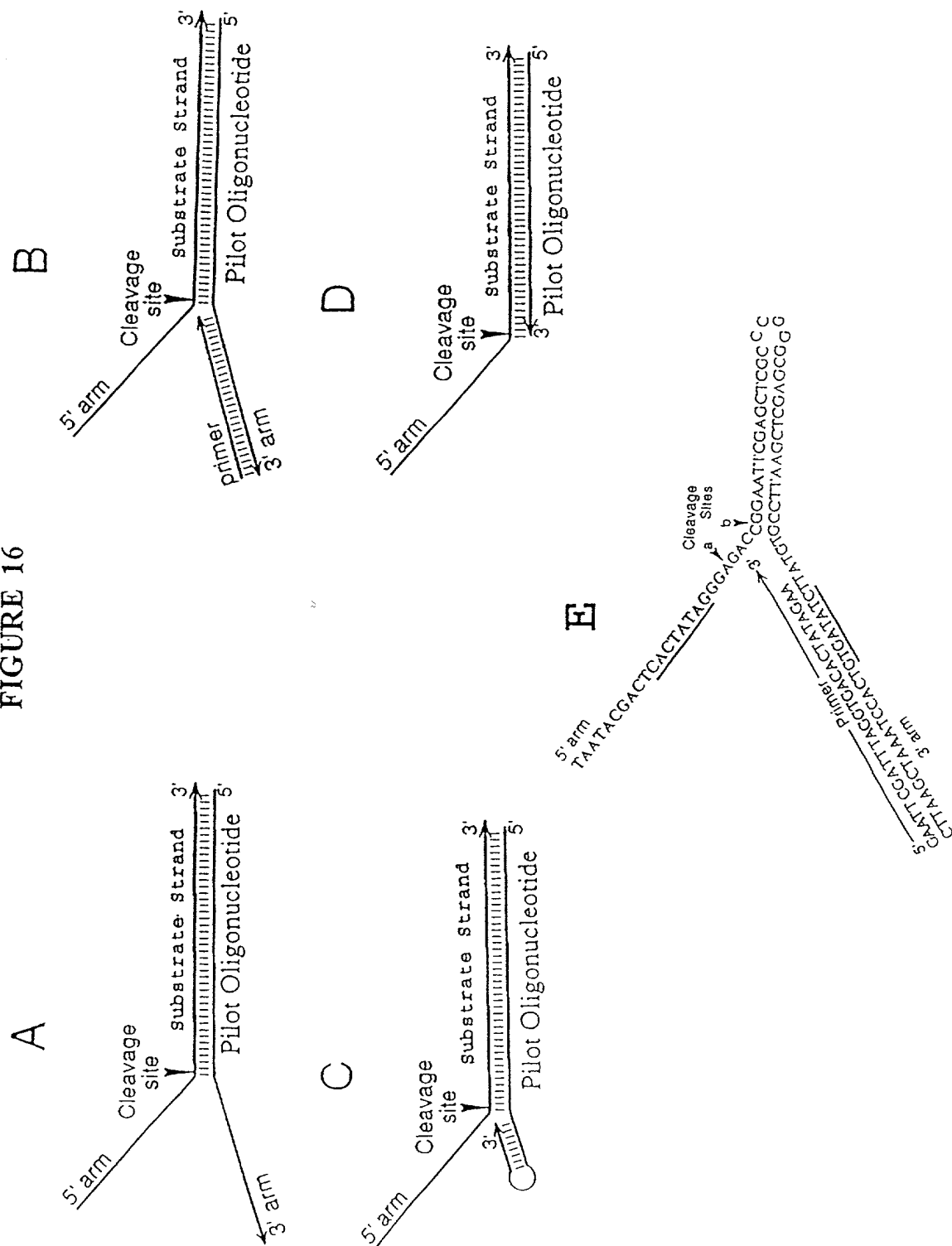


FIGURE 17

1 2 3 4 5 6 7

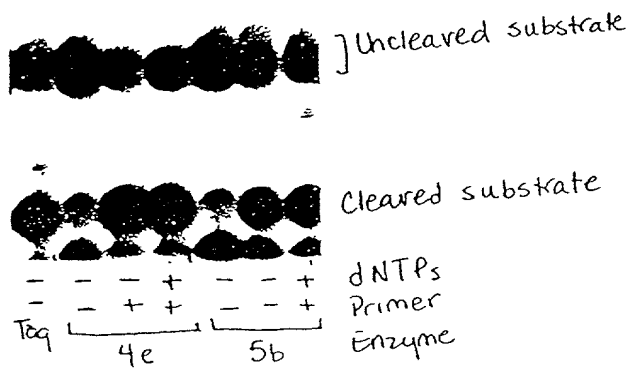


FIGURE 18

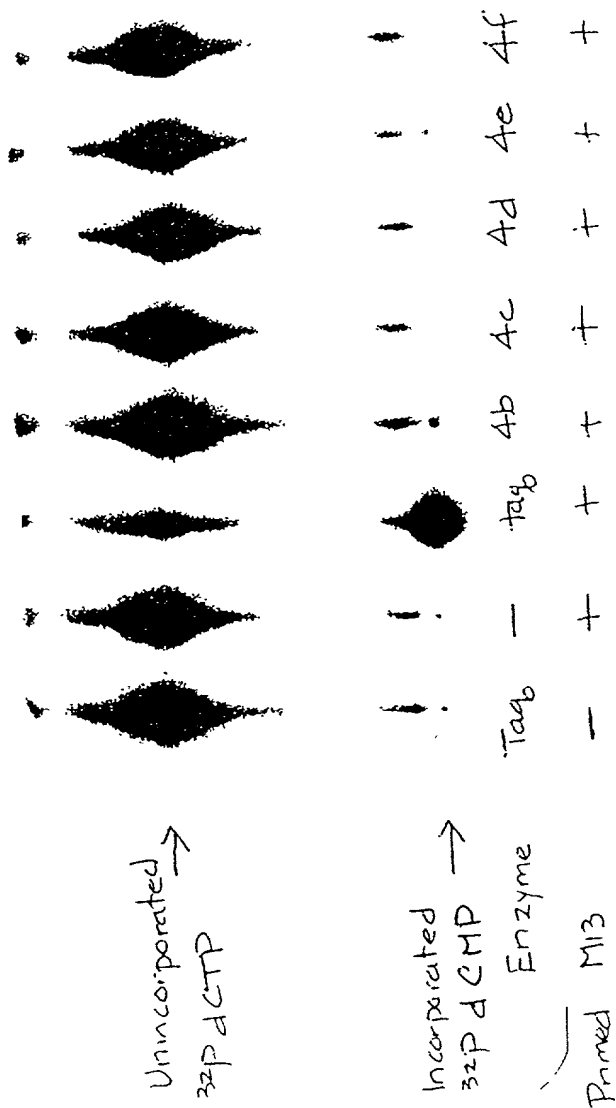
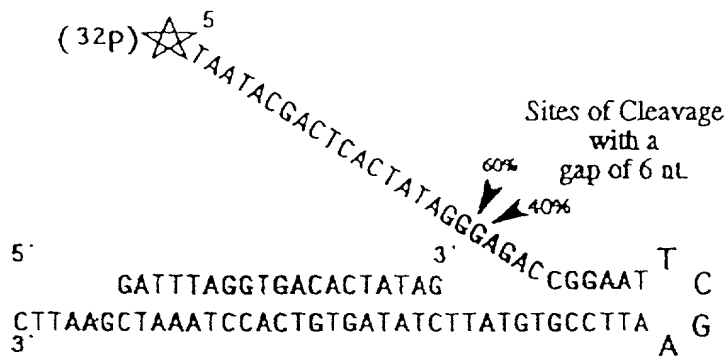


FIGURE 19



A




B

		"4d"		"4b"			
		No mutation		(2 pt. mutation)		Unmodified	
		Pol. Activity		small activity		DNAP Tag	
1	2	3	4	5	6	7	8
		C/A		T/A		T/A	
		+		-		+	

ATP

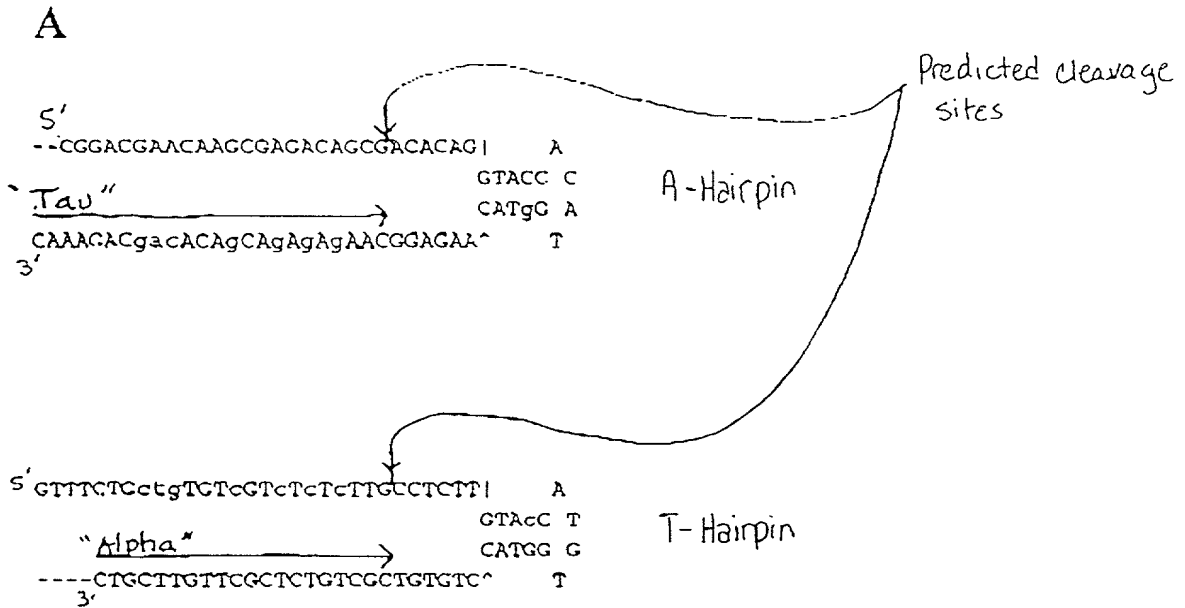
84 nt —  —  ← hairpin test molecule
 ← conversion to double stranded.
 (complete extension of primer)

desired product
 21 nuc.

 } Multiple bands caused by polymerization

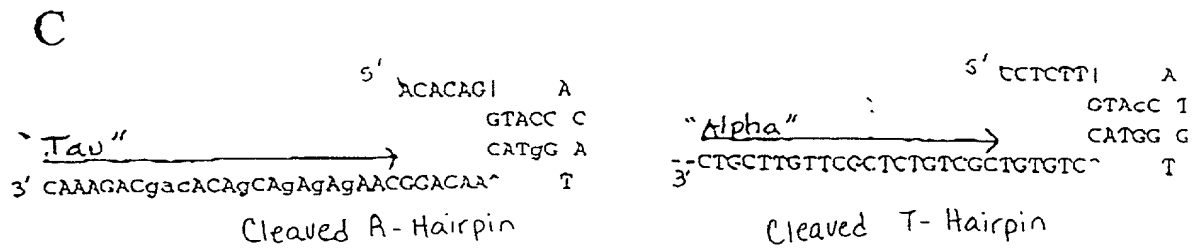
↑ some aberrant cleavage with "4b" because of residual polymerase activity.

FIGURE 20



B Sequence of alpha primer:

5' GAC GAA CAA CCG AGA CAG CG 3'



D

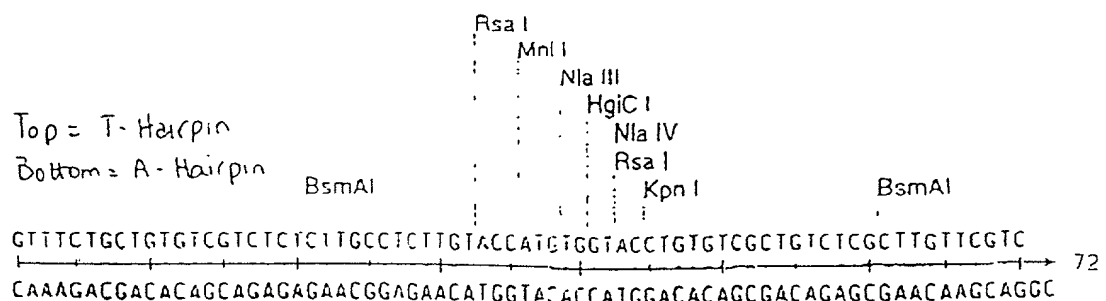


FIGURE 21

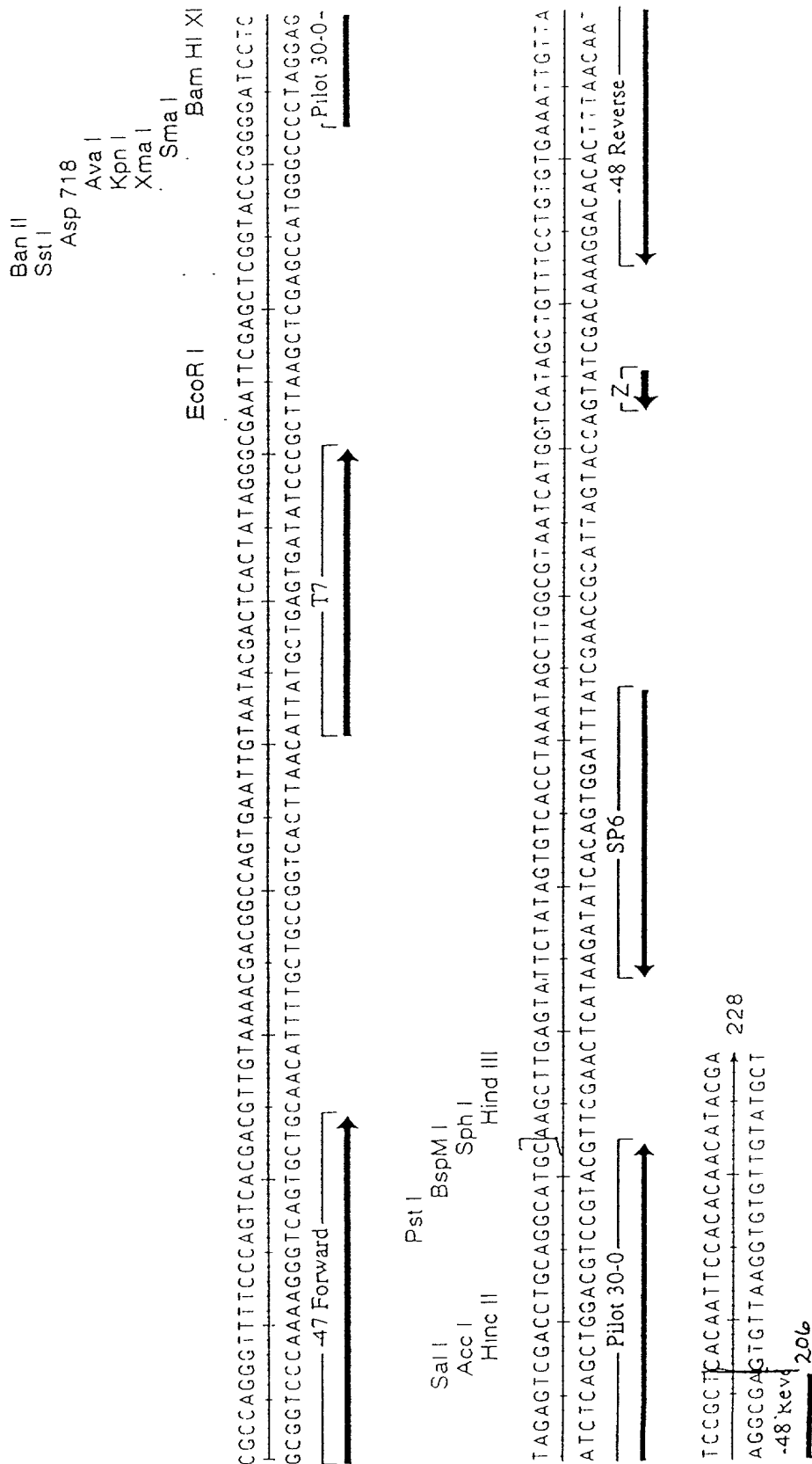


FIGURE 22A

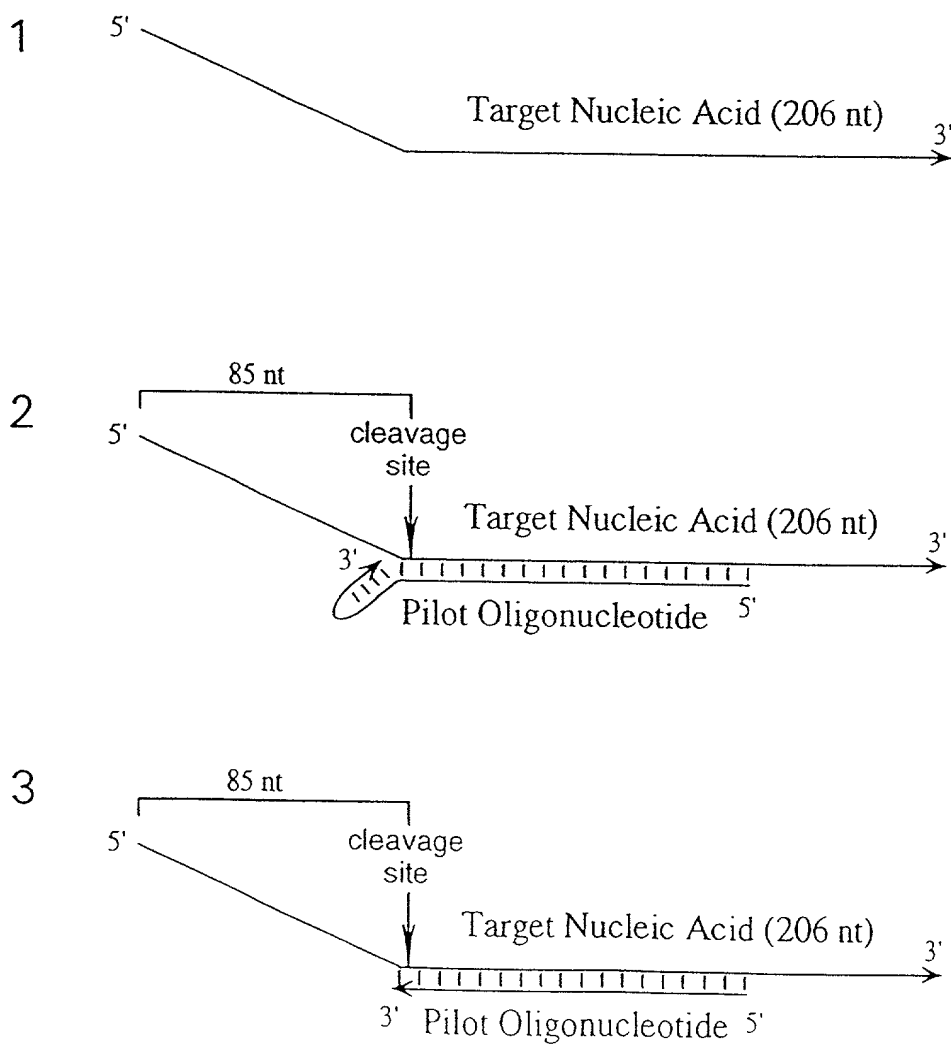


FIGURE 22B

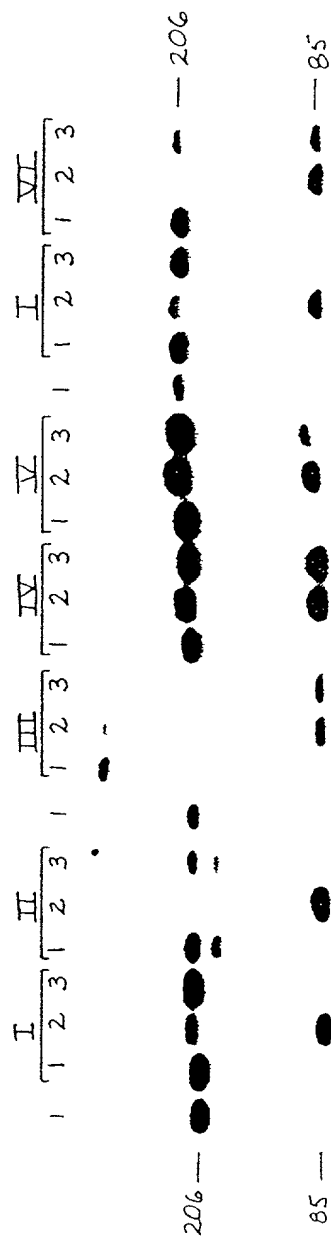


FIGURE 25

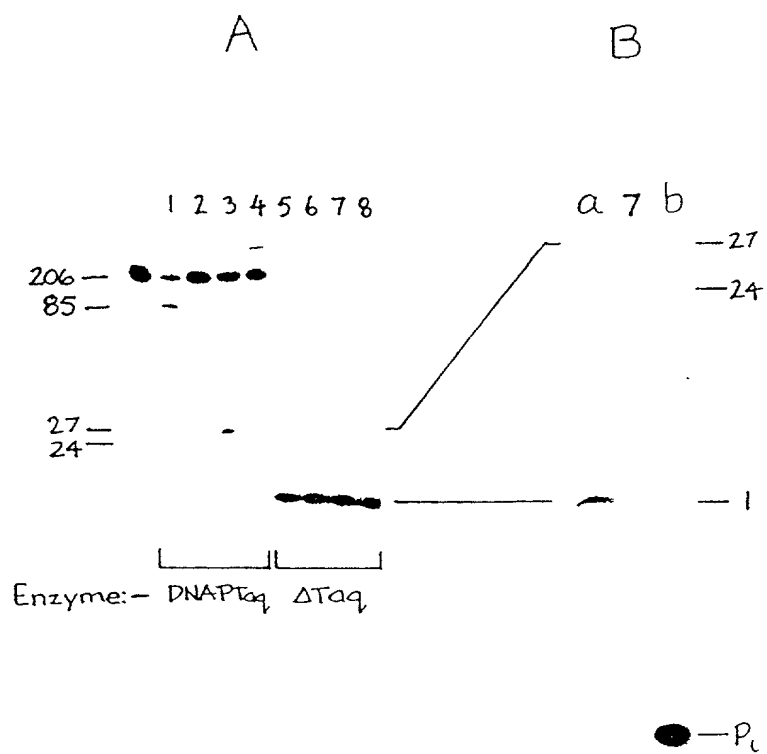
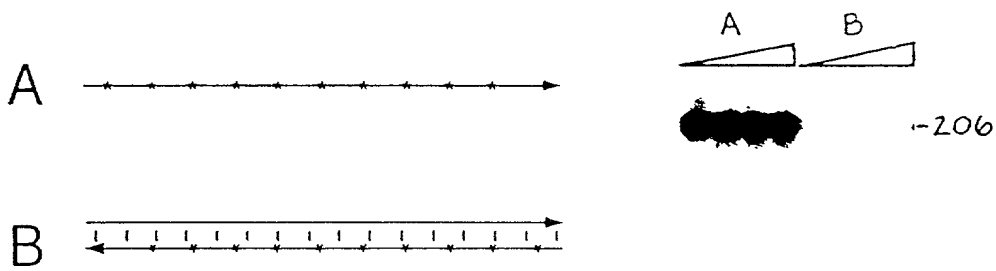


FIGURE 26



* = ^{32}P

FIGURE 27

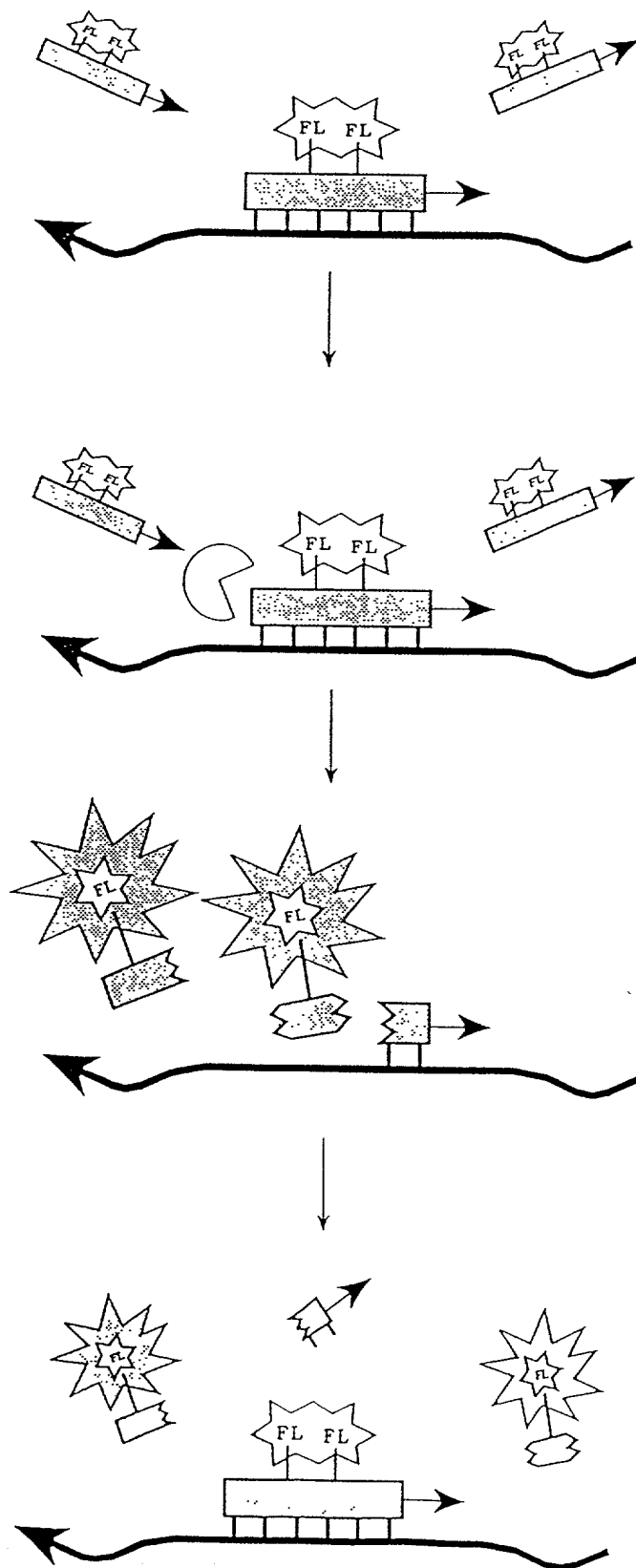
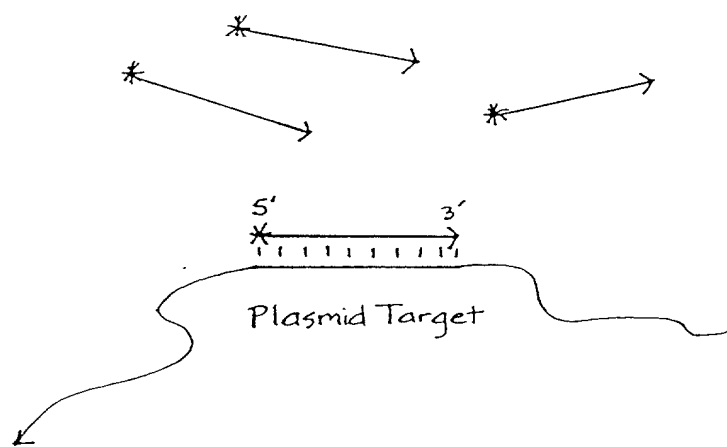


FIGURE 28A



* = ^{32}P 5' terminal phosphate

40074323 024007

FIGURE 28B

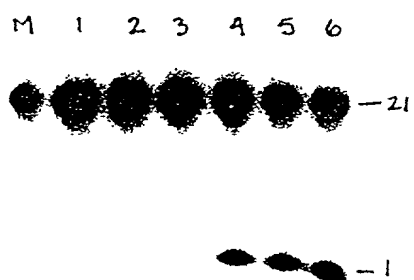


FIGURE 29

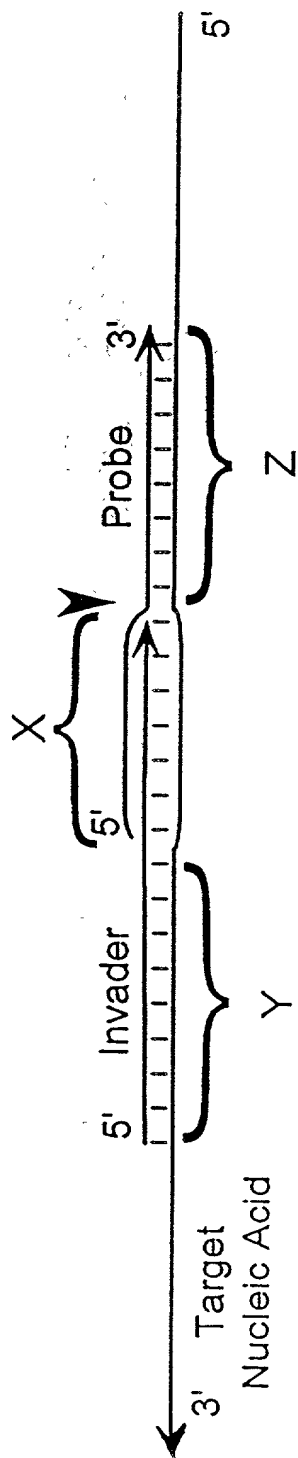


FIGURE 30

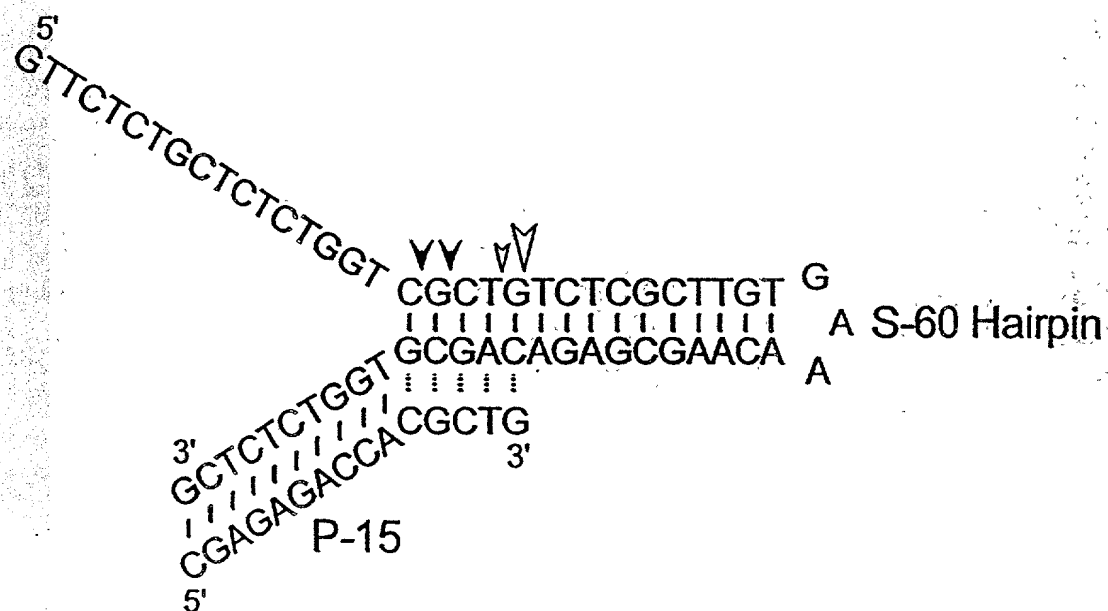


FIGURE 31

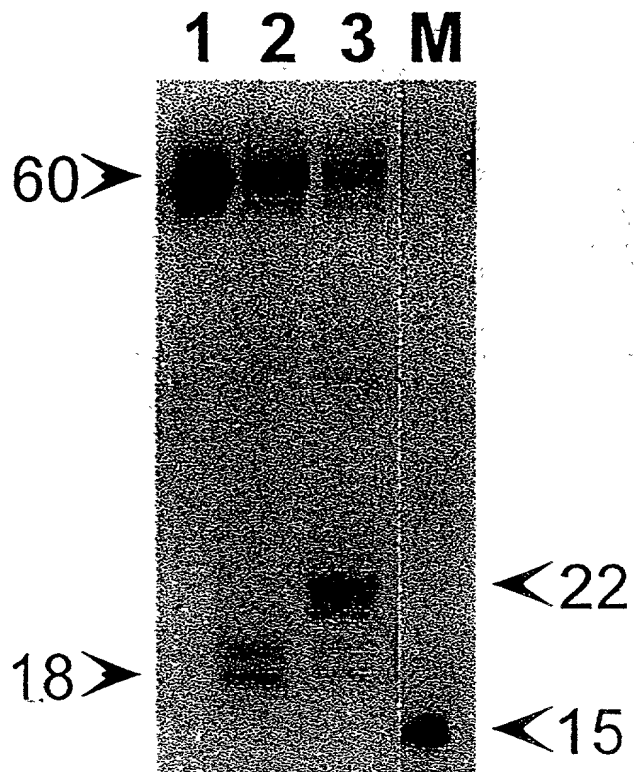
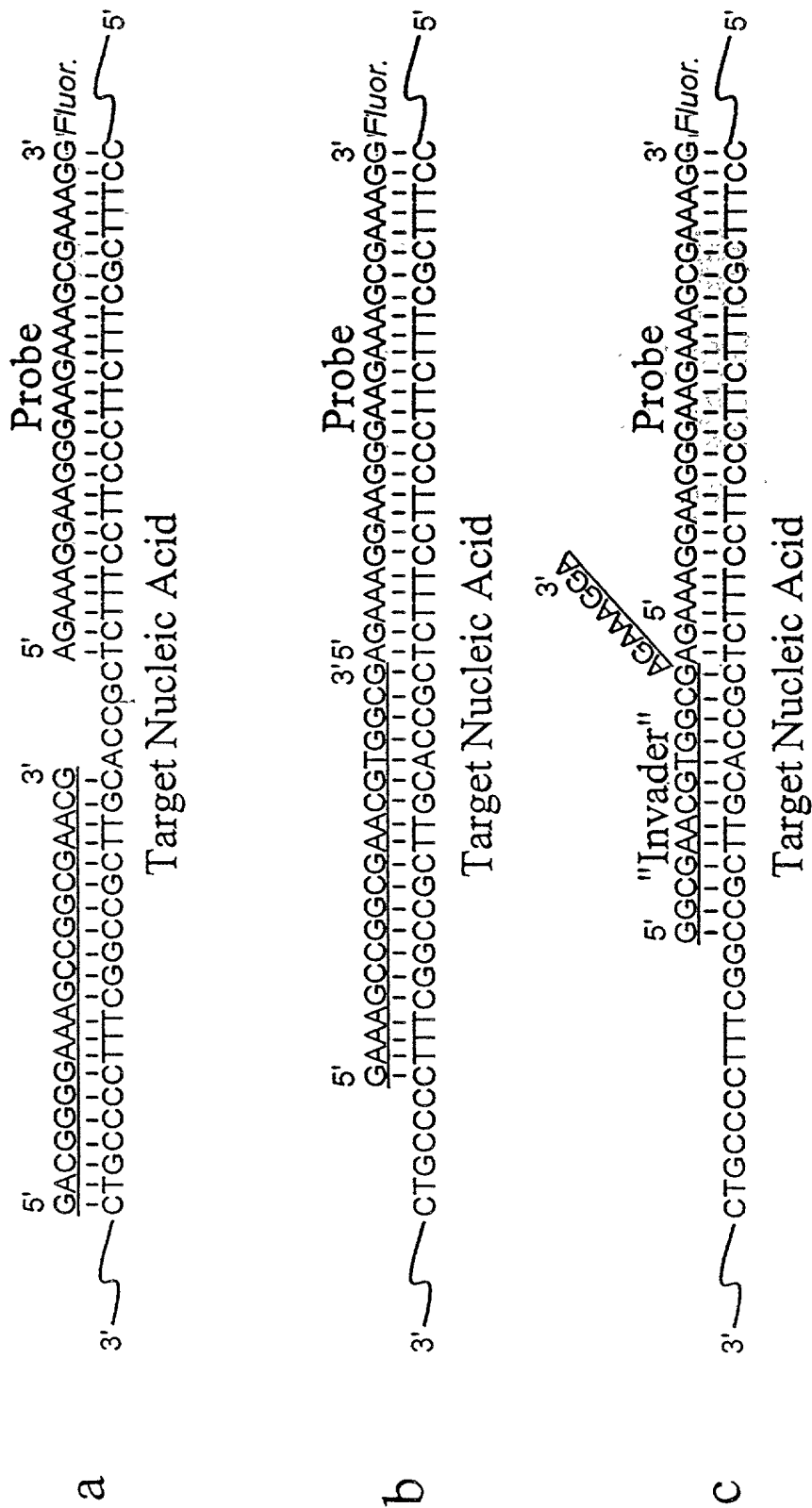


FIGURE 32
"Invader" Sequences



44

202120" 82E41001

8

7

6

5

4

3

2

1

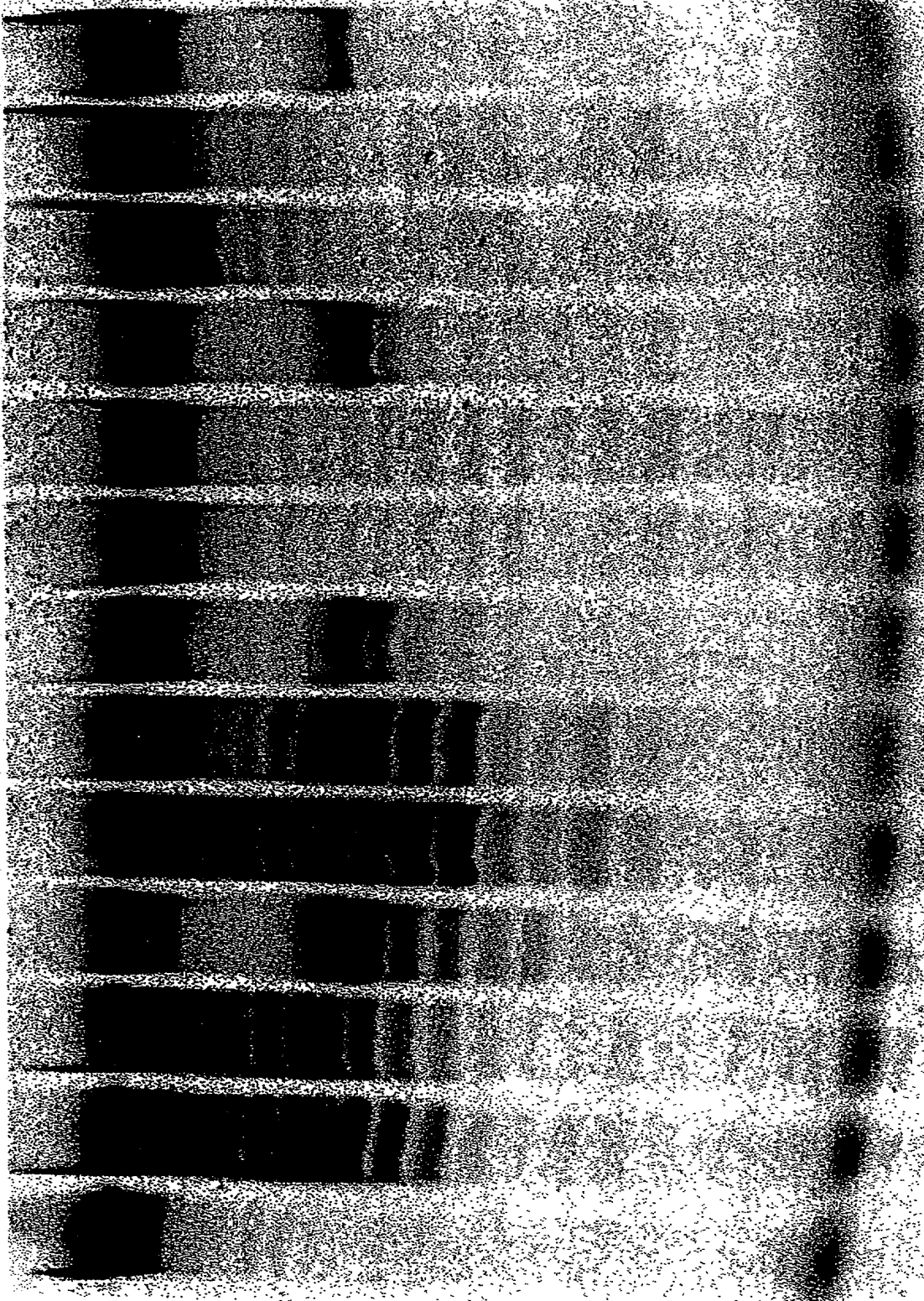
267

45

FIGURE 34

202120" 82E4/00T

M 1 2 3 4 5 6 7 8 9 10 11 12

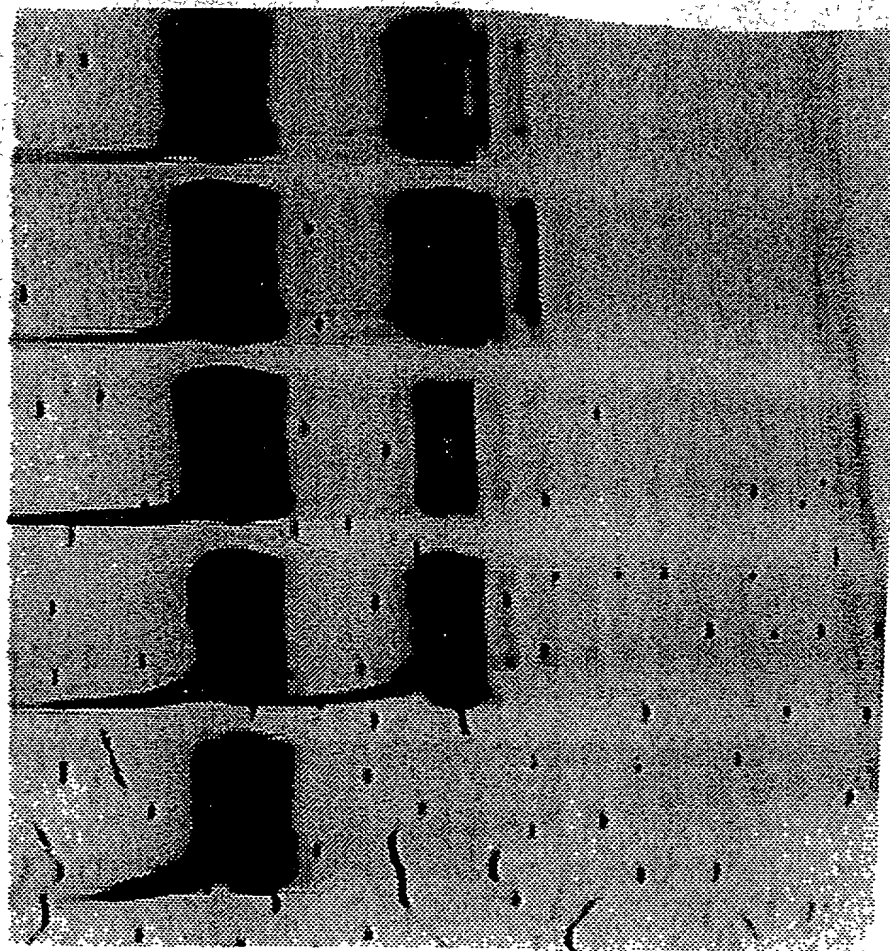


26

46

202120" B2E4/001

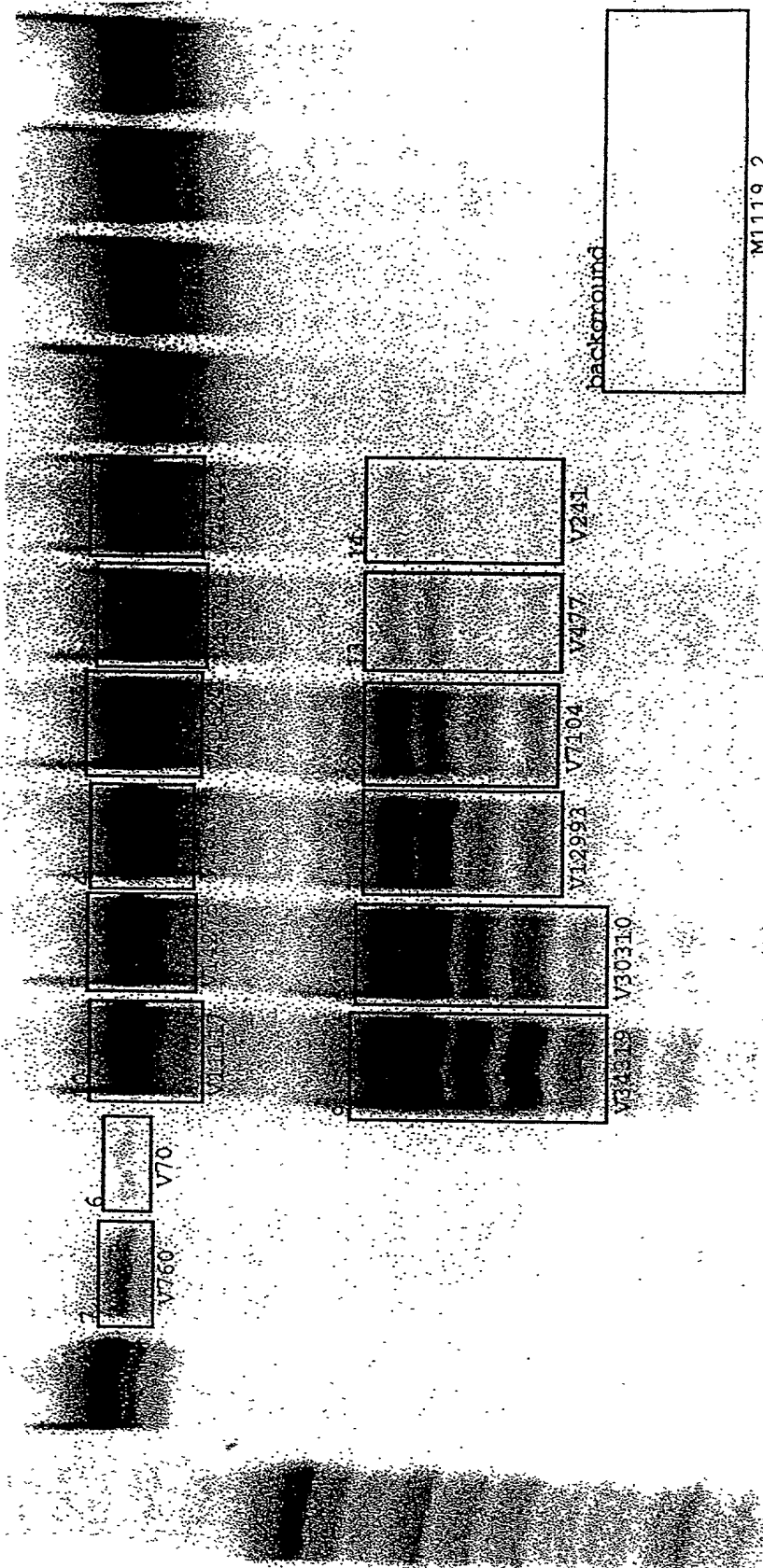
1 2 3 4 5



26

FIGURE 36
202120" B2E4/001

M 1 2 3 4 5 6 7 8 9 10 11 12 13



10074328 02E47001

1 2 3 4 5 6 7 8 9 10 11

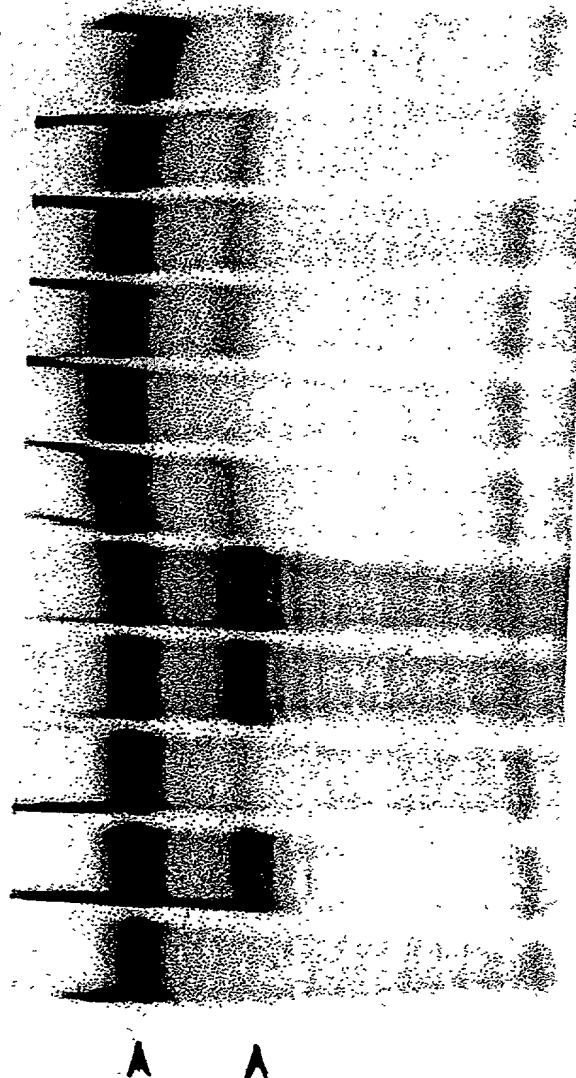


FIGURE 38 E2E4/2001

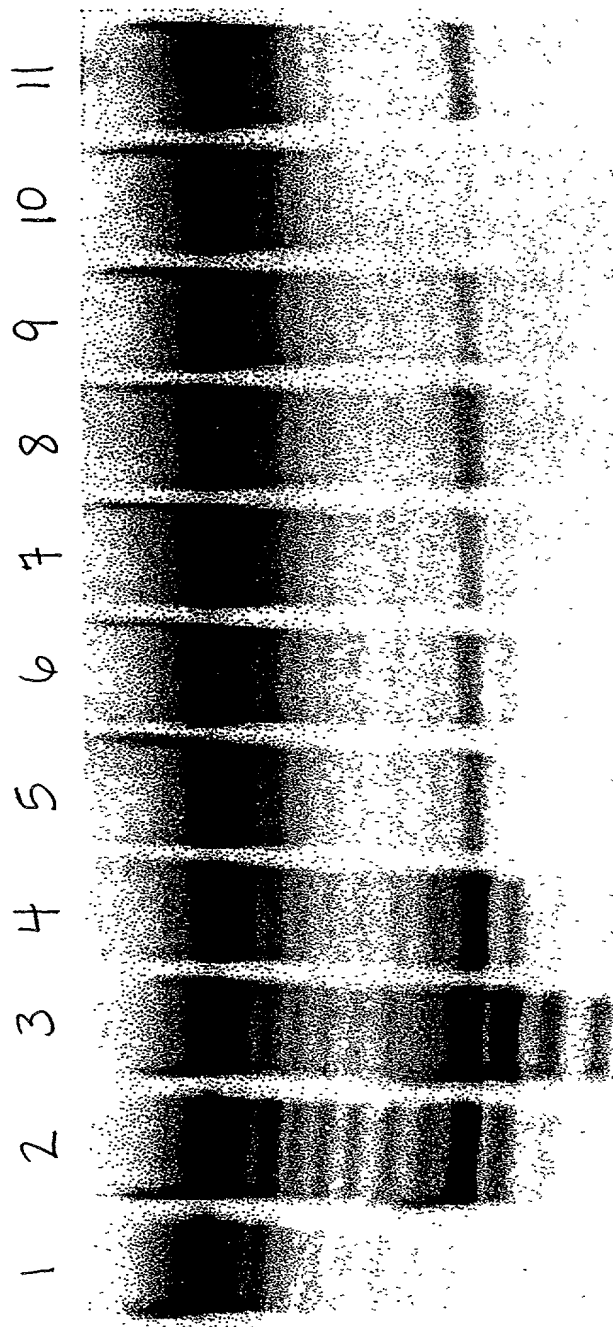


FIGURE 39

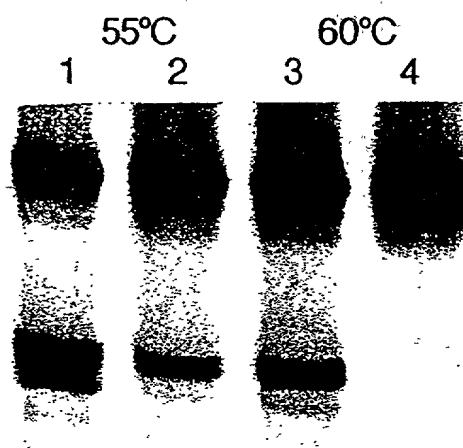


FIGURE 40

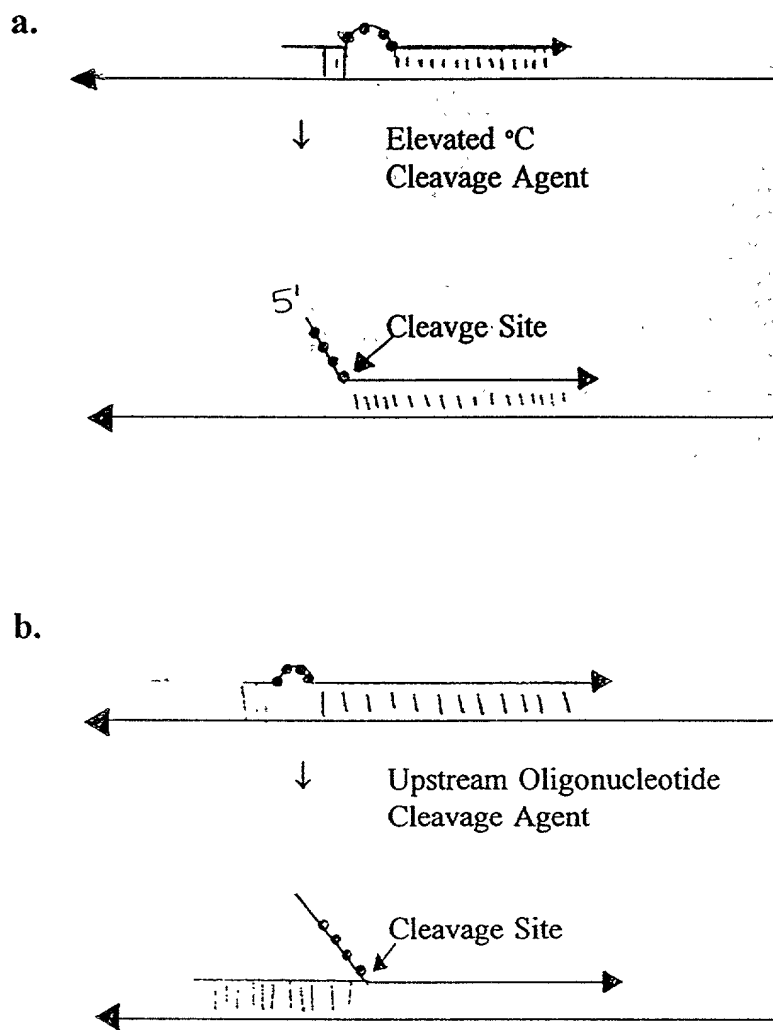


FIGURE 41

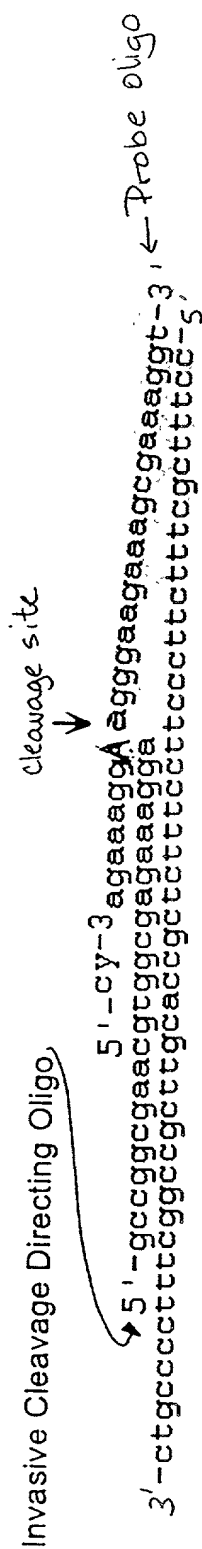


FIGURE 42

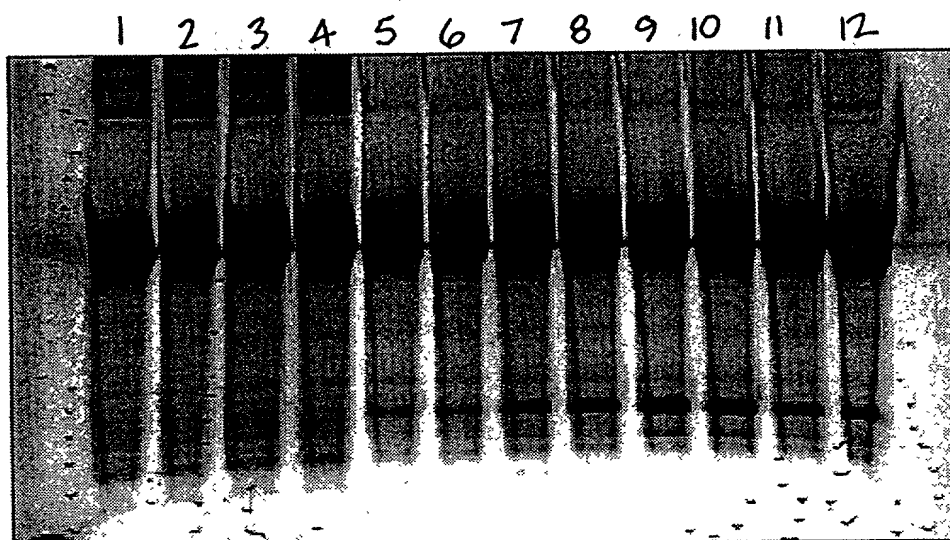
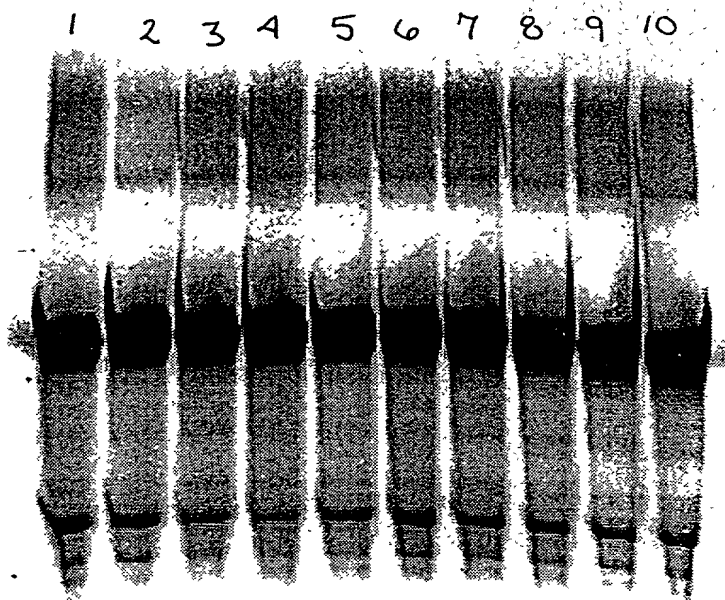


FIGURE 43



SS

FIGURE 44

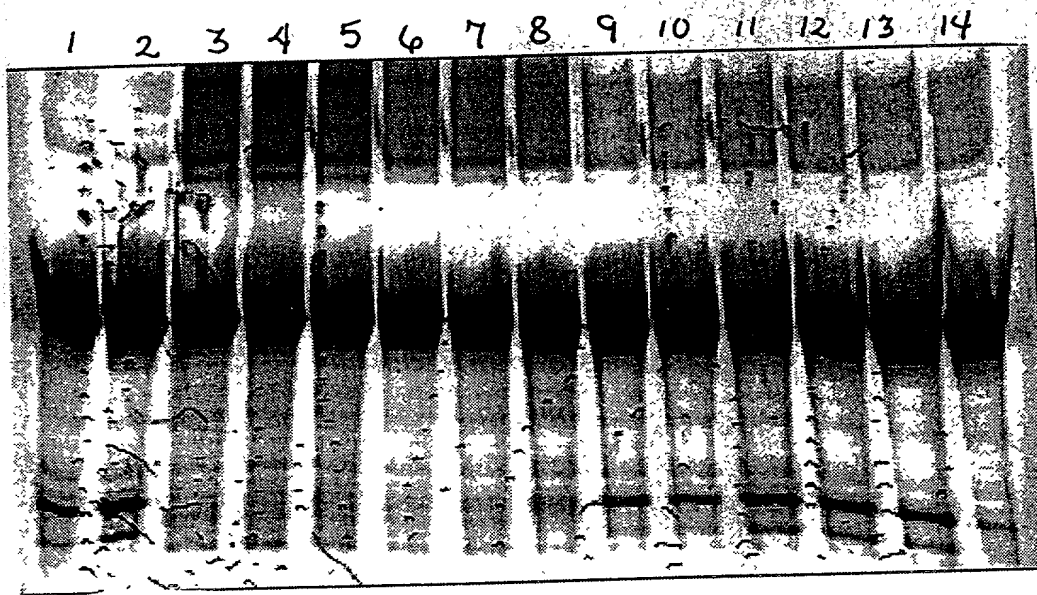


FIGURE 45

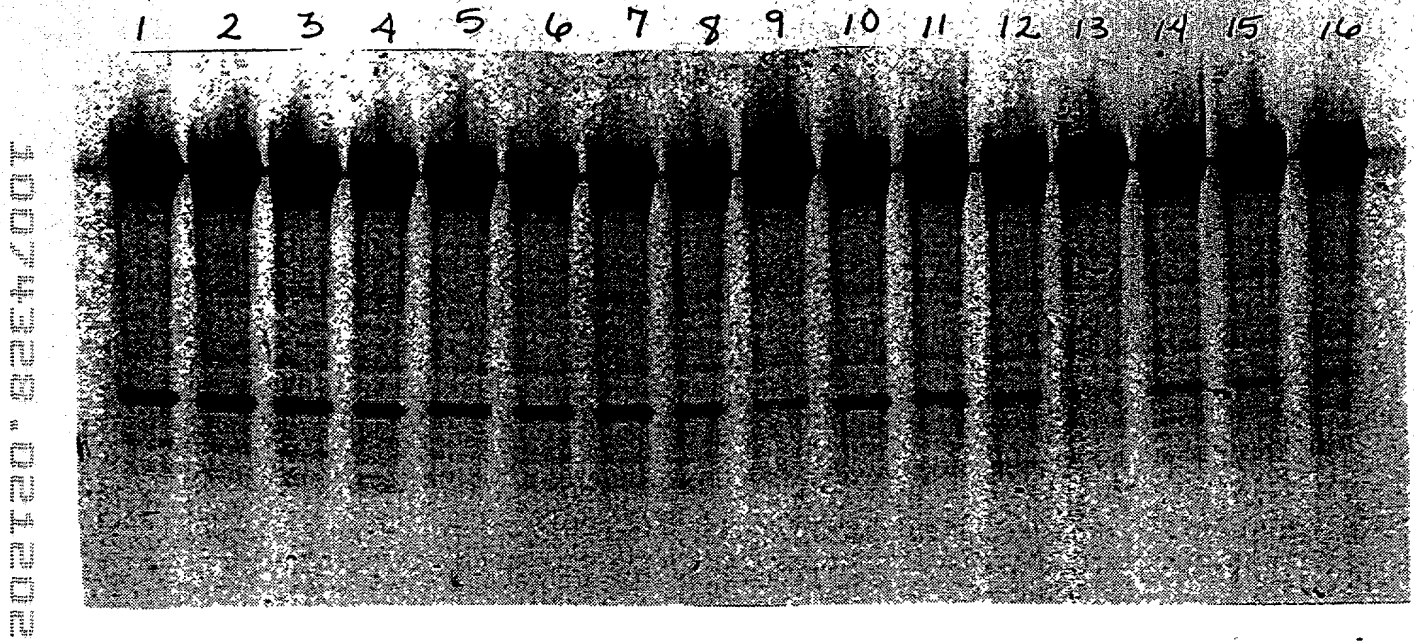
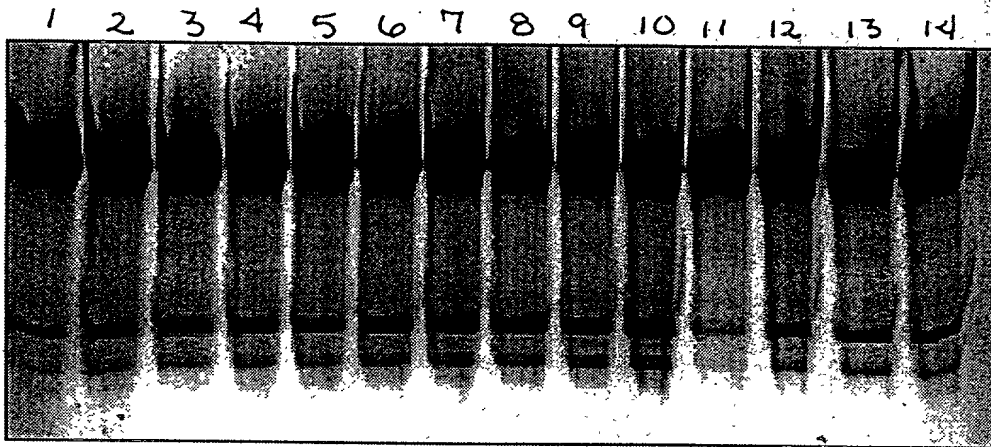


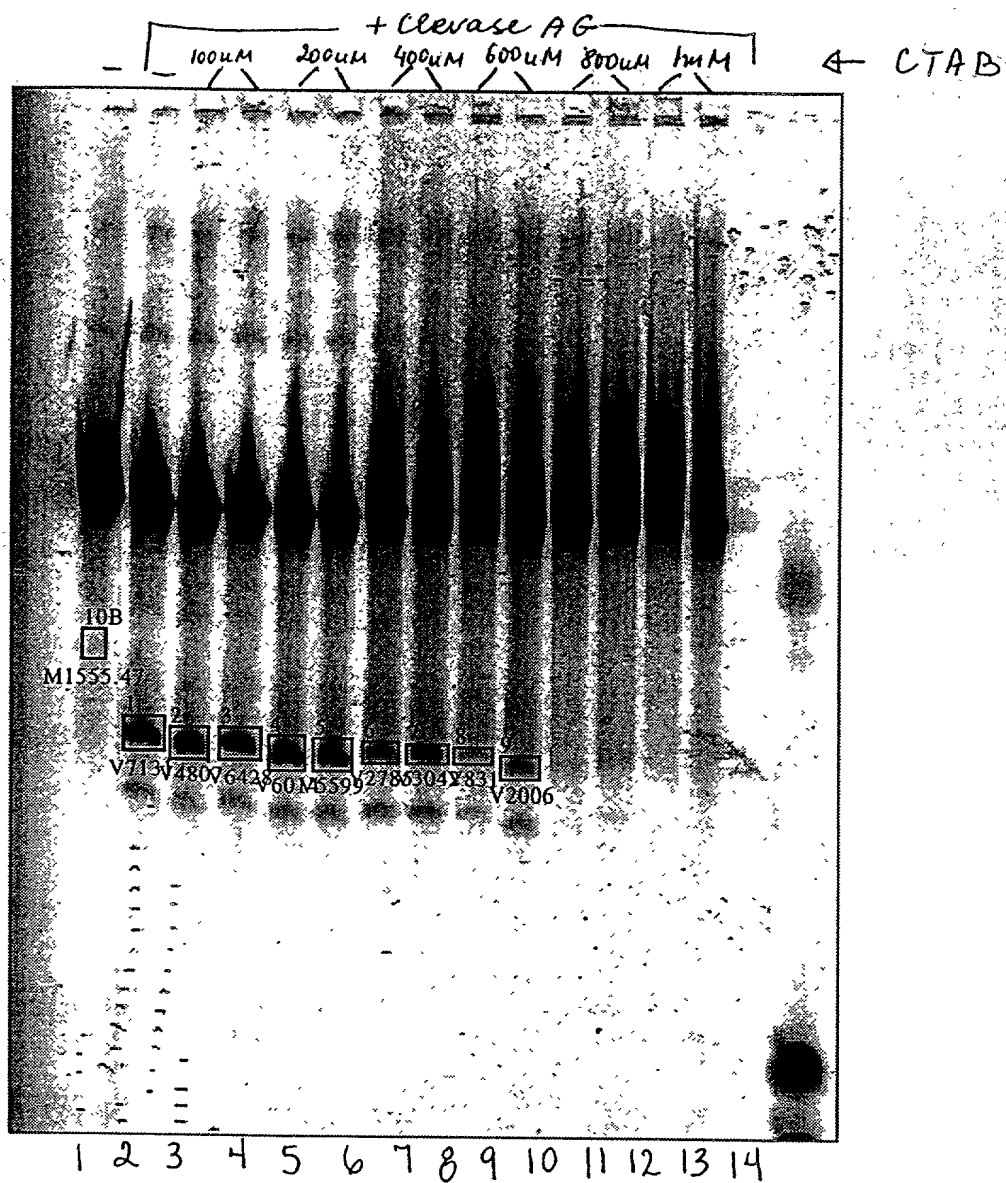
FIGURE 46



10074323, 021203
202120" 8254/001

58

FIGURE 47



59

202120" 32E42001

FIGURE 48

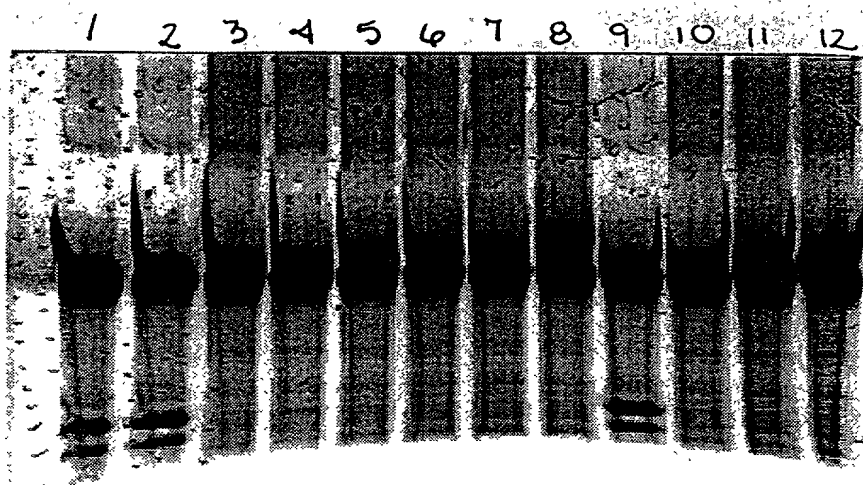
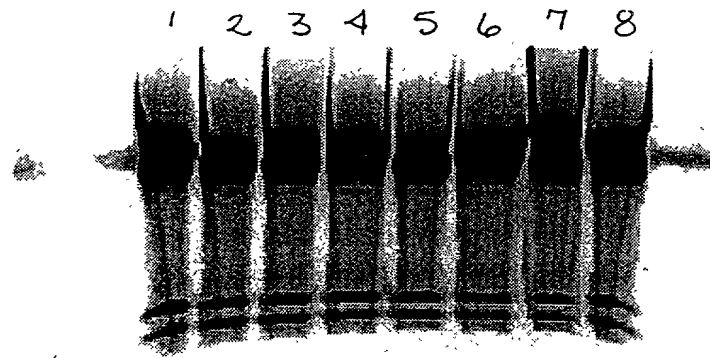
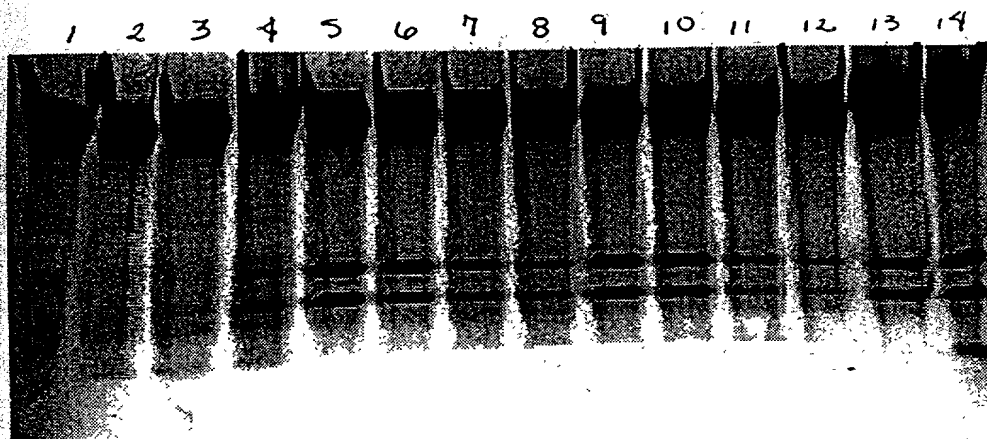


FIGURE 49



10044938.024202
202120" BEEH/001

FIGURE 50



2021 20 32E4/001

FIGURE 51

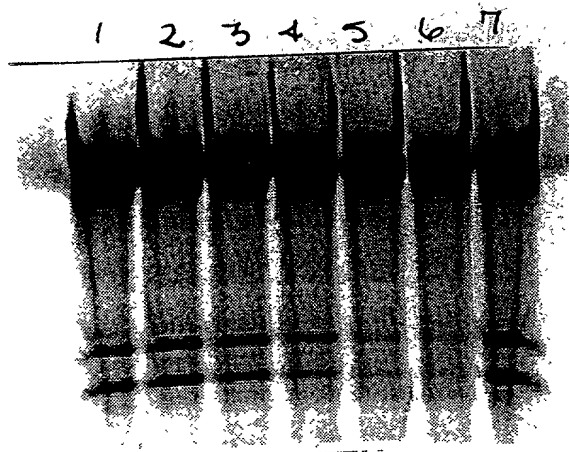
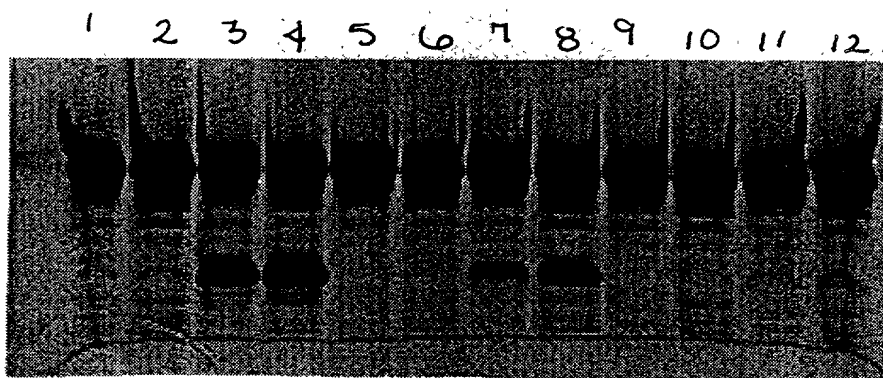


FIGURE 52

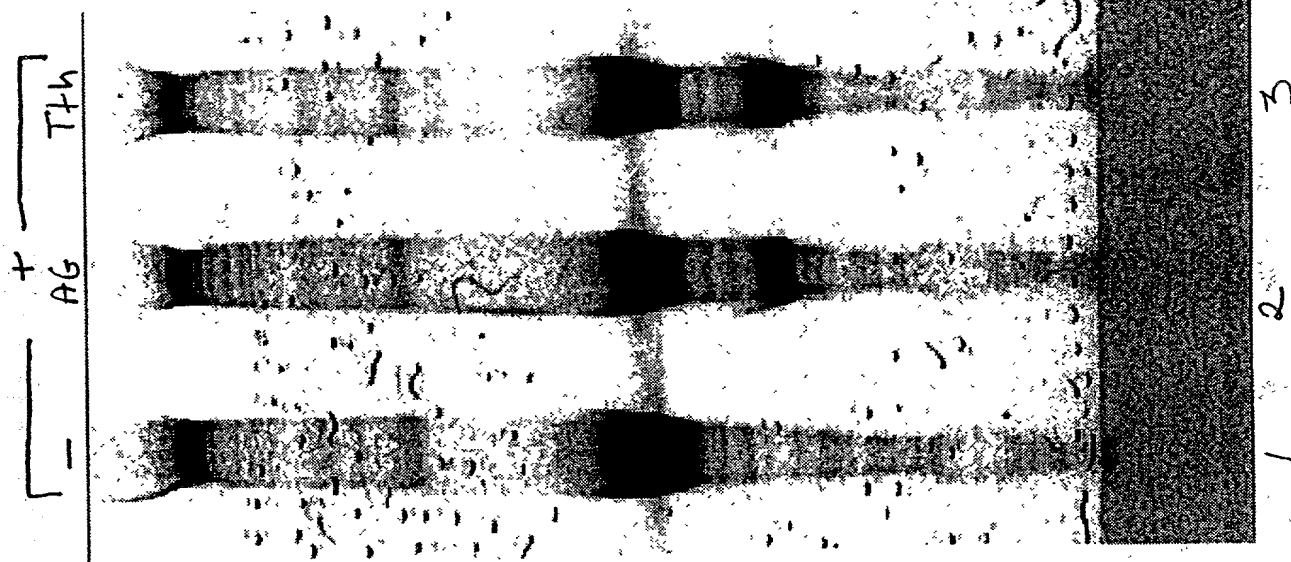


202120" B&H/OUT

64

FIGURE 532 E4001

a



b

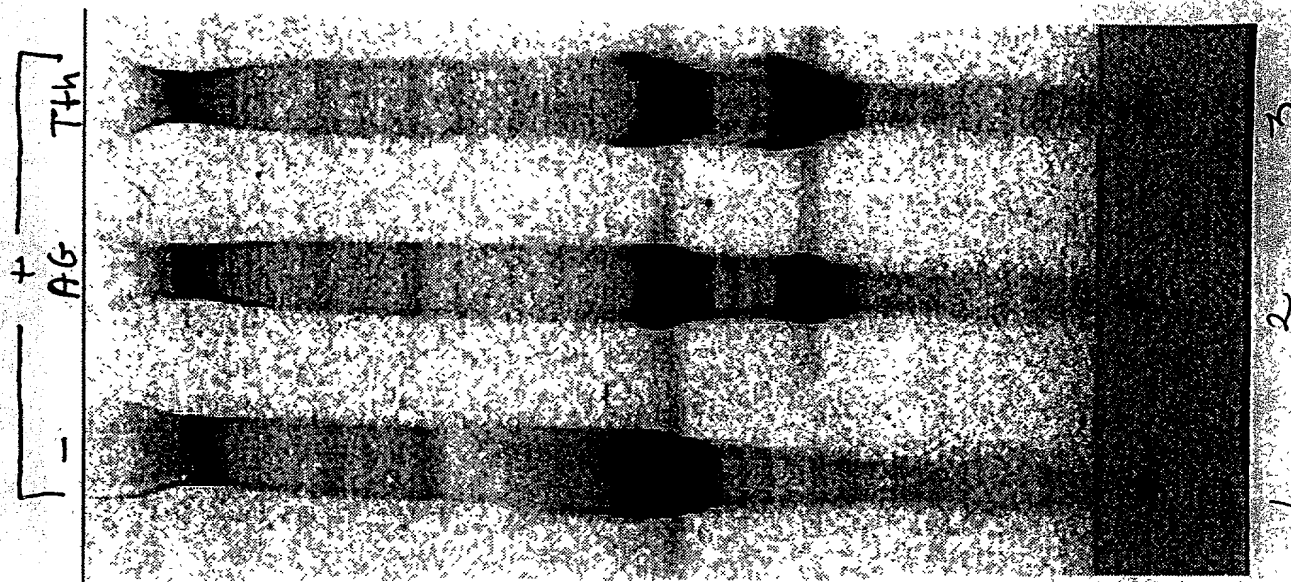


FIGURE 54

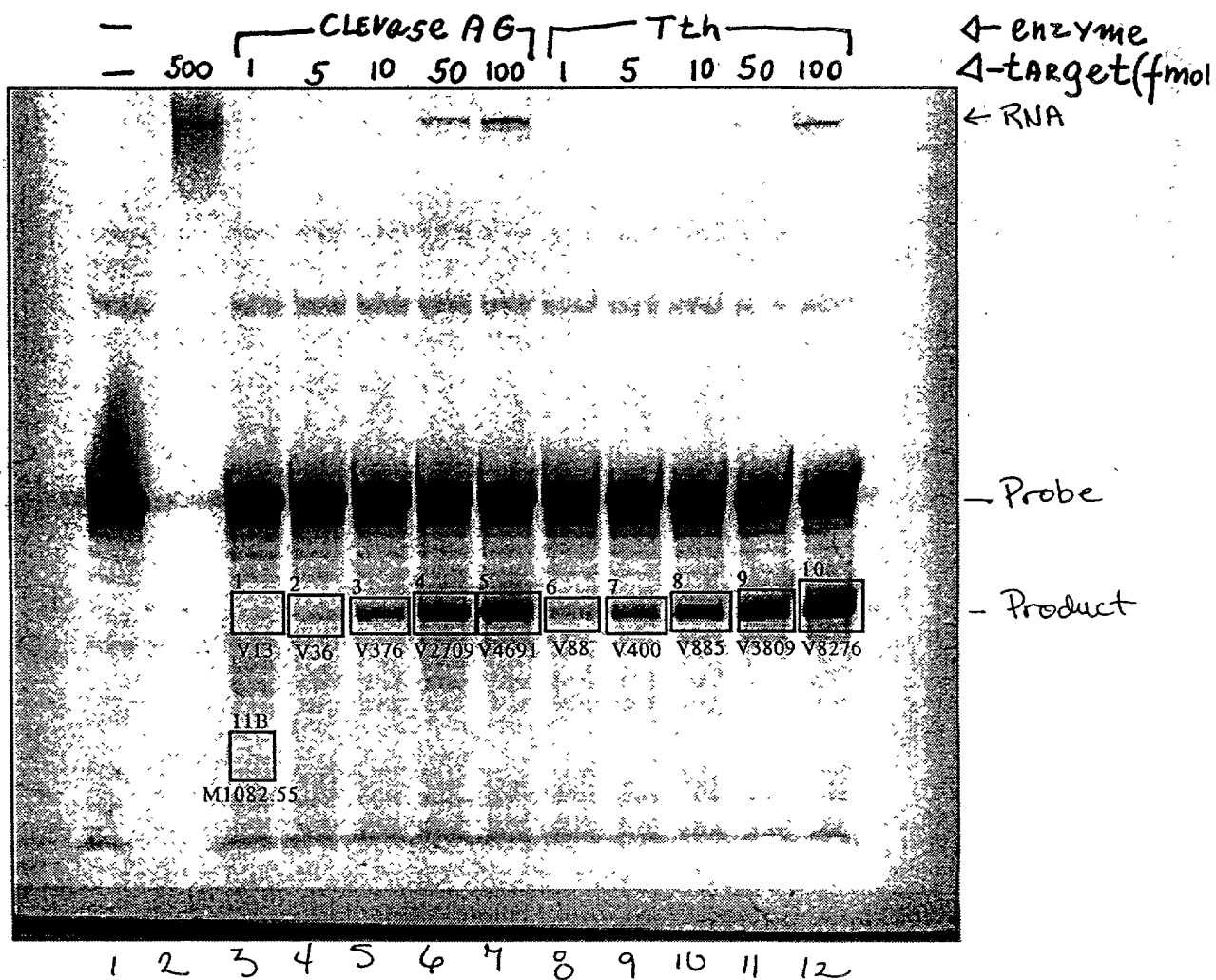


FIGURE 55

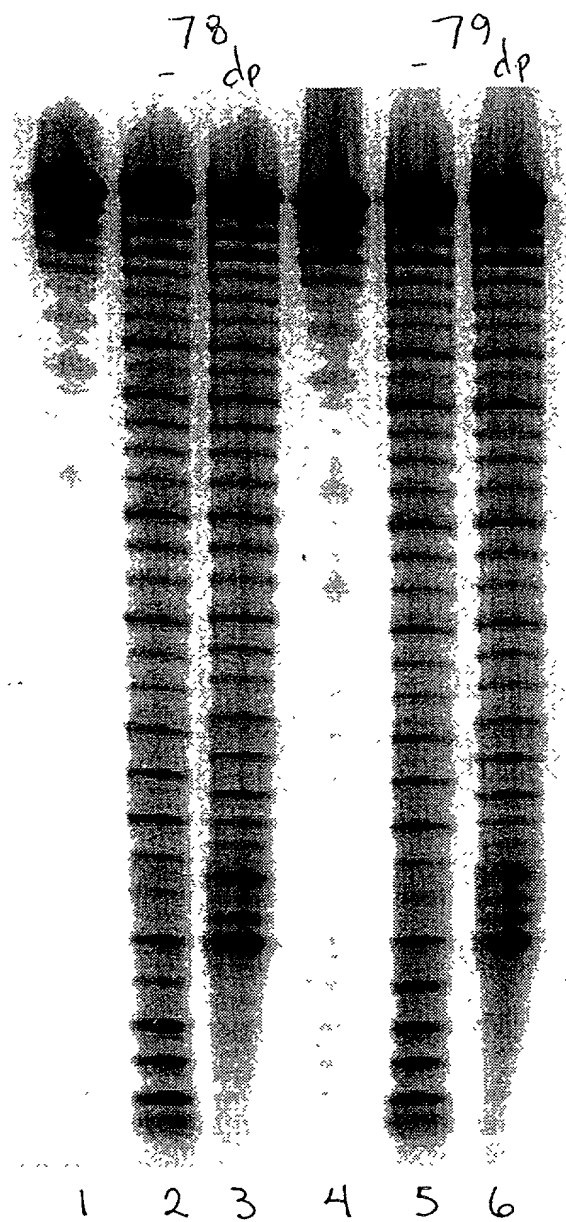


FIGURE 56

70 (C10 aminoT's)

74 (C6 amino T's)

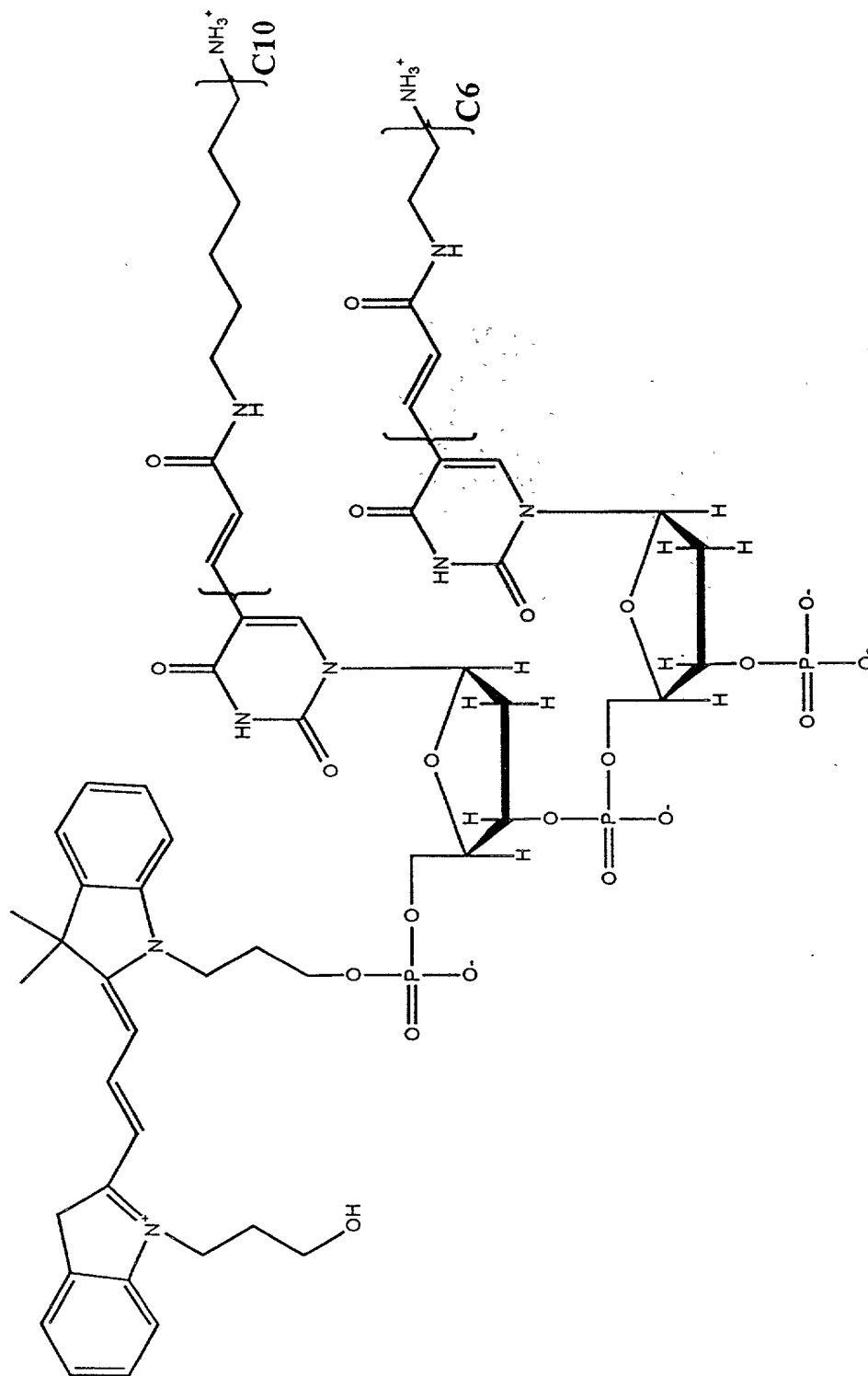
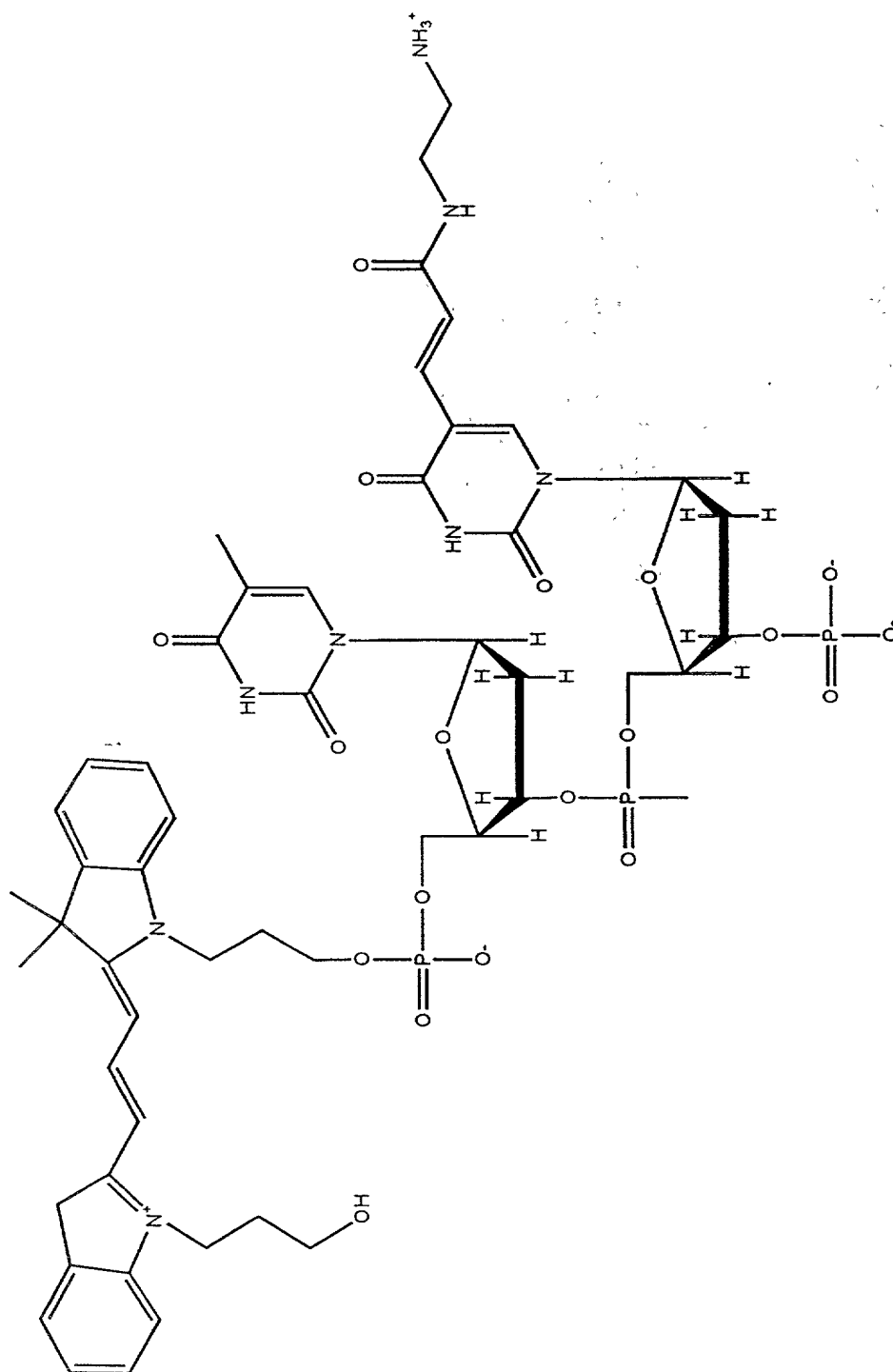
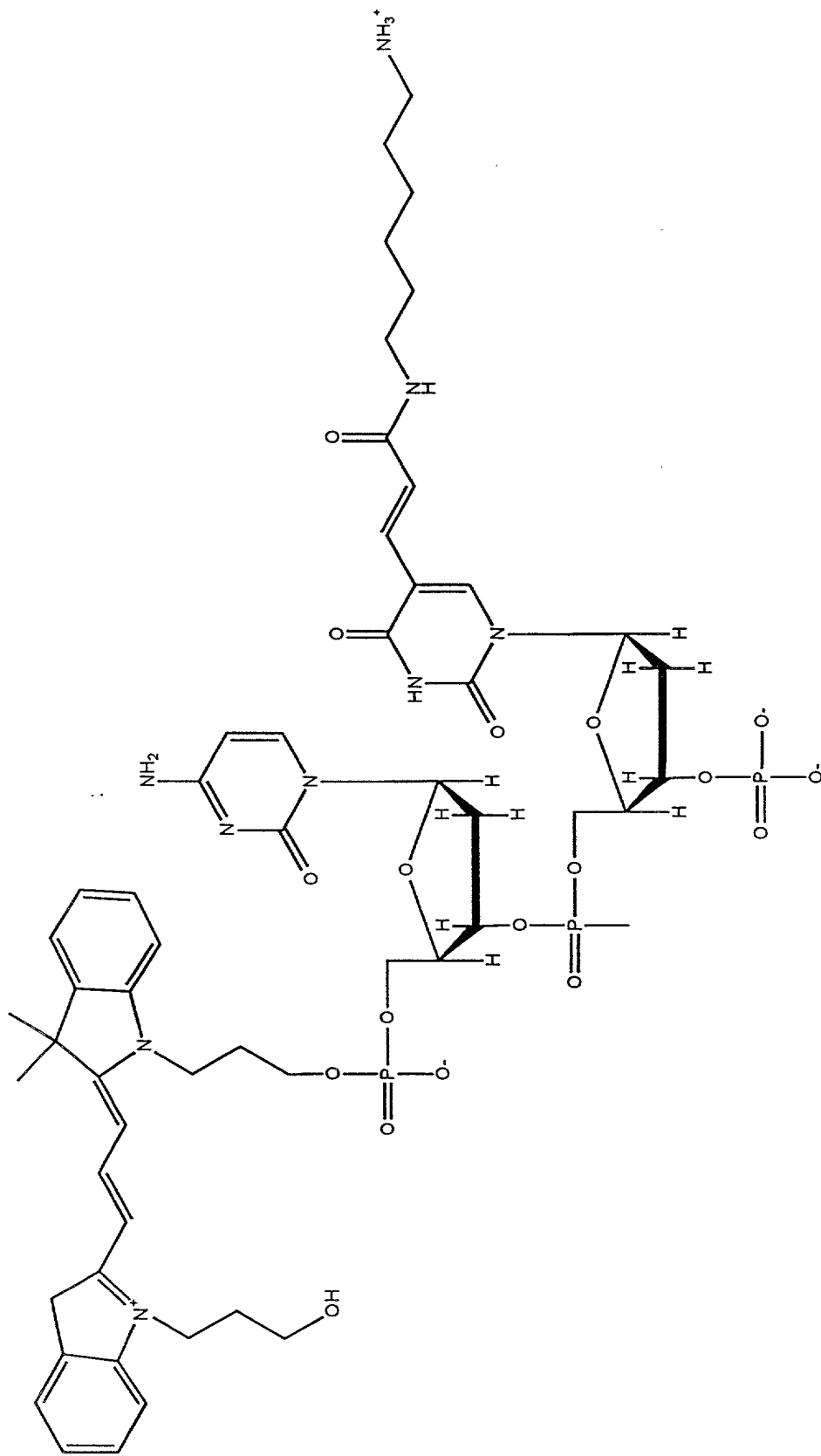


FIGURE 57

75



69



70

FIGURE 59

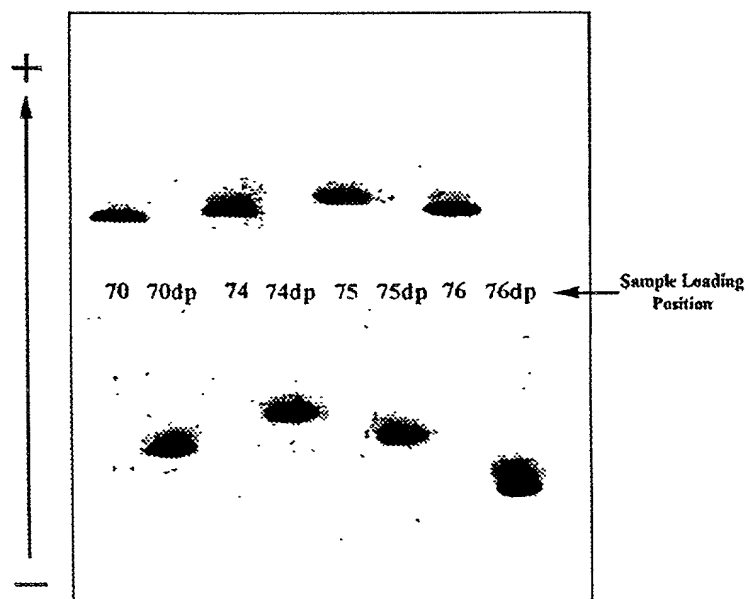
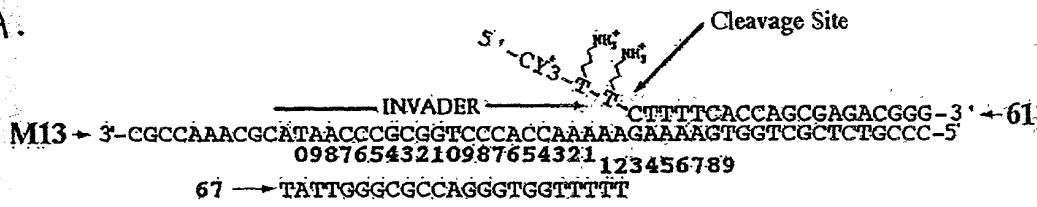


FIGURE 60

A.



B.

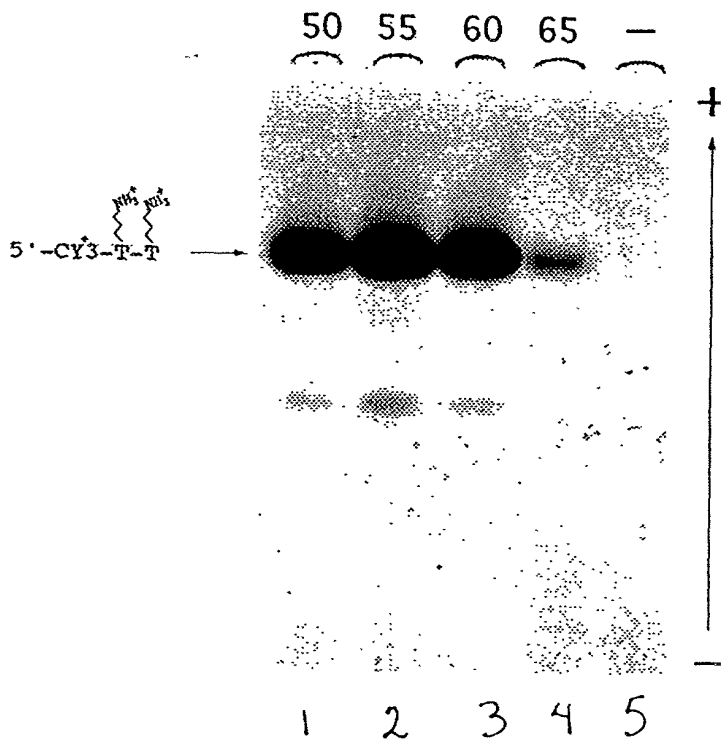


FIGURE 61

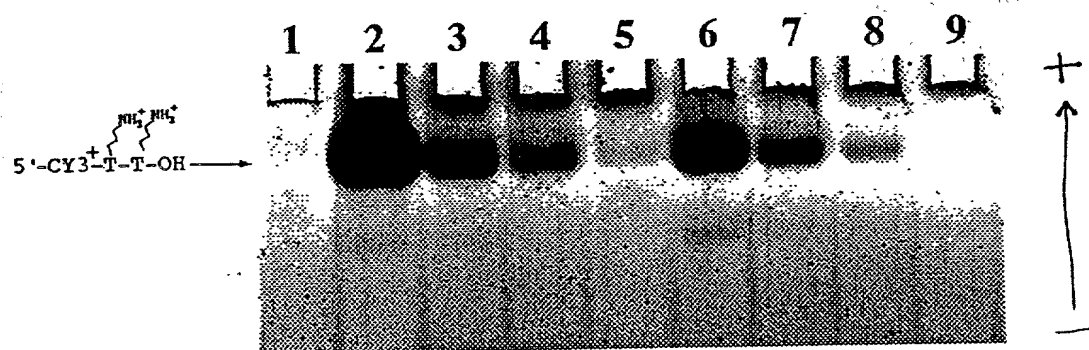


FIGURE 62

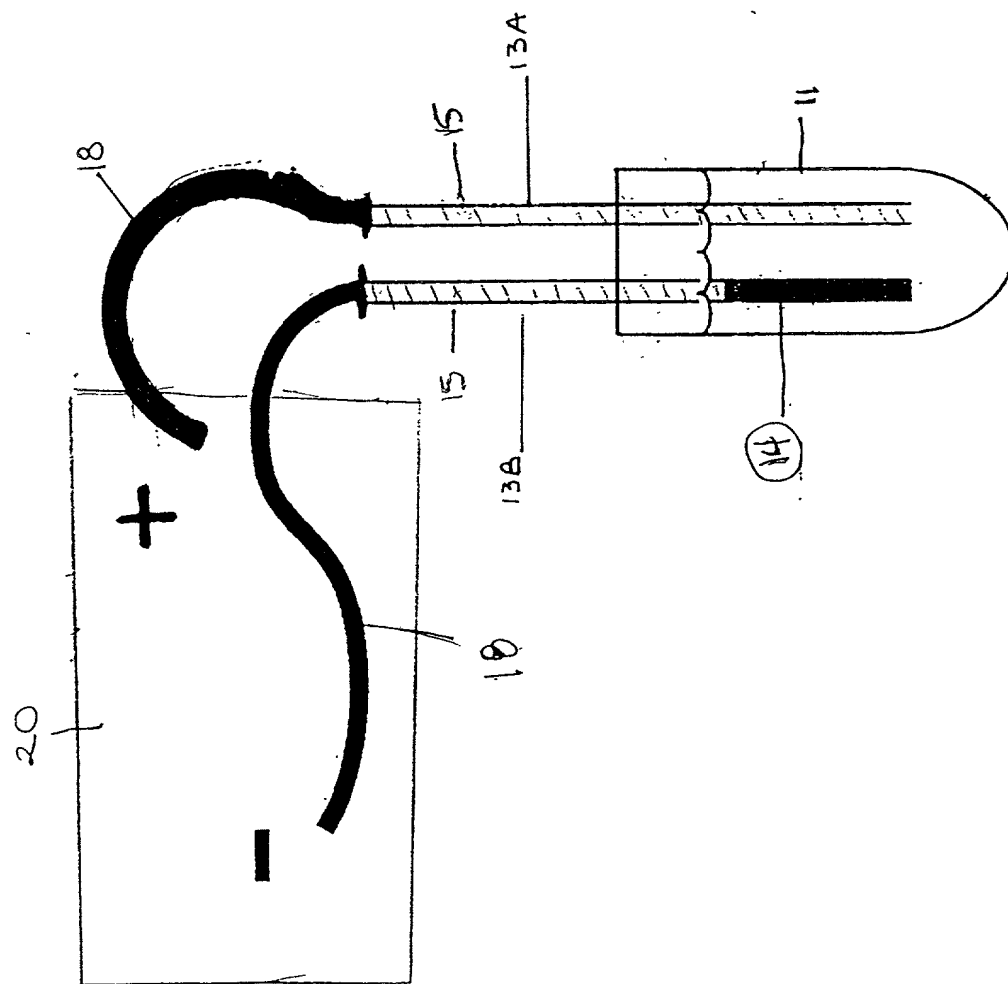
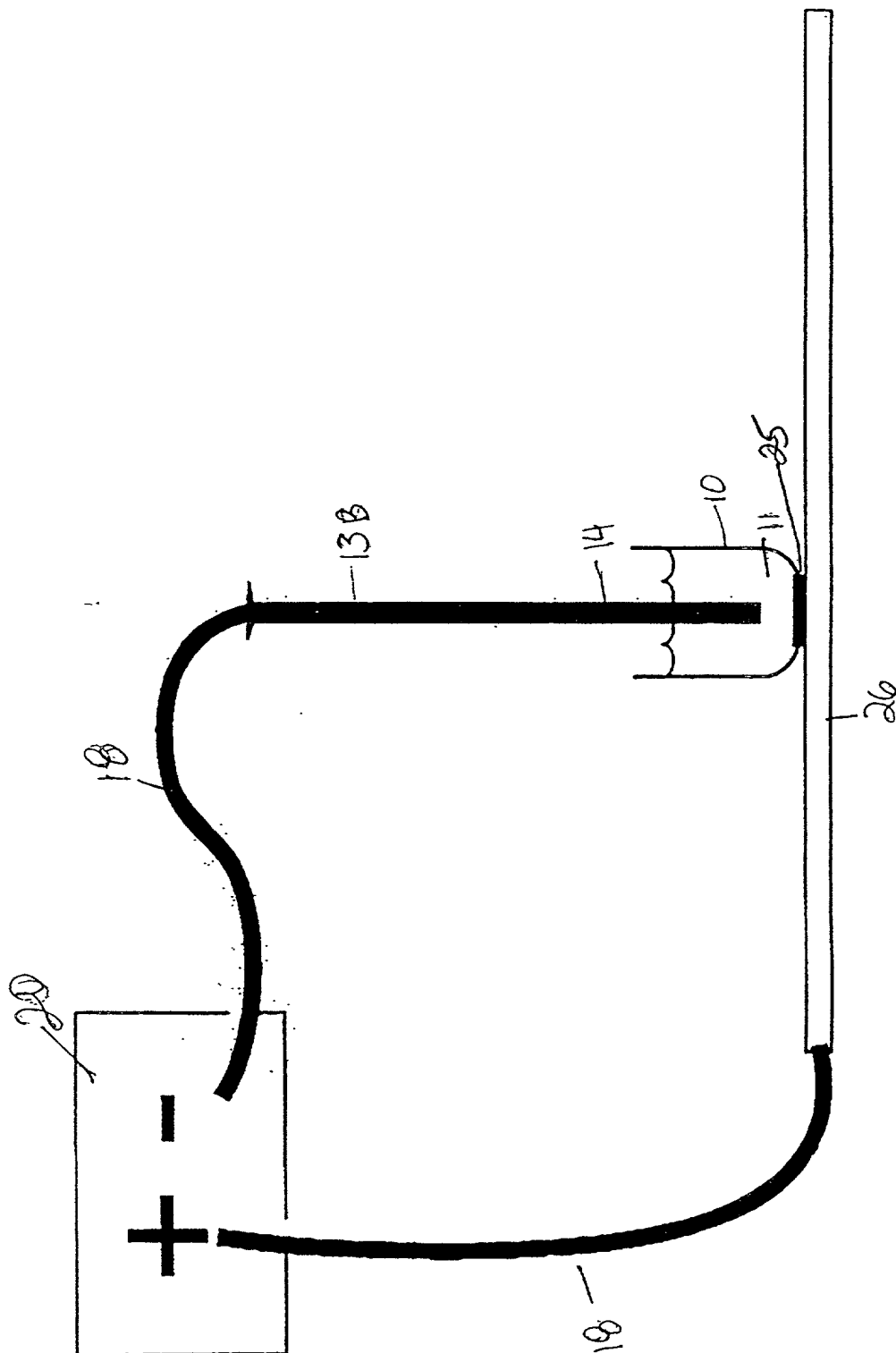


FIGURE 63



57

FIGURE 64

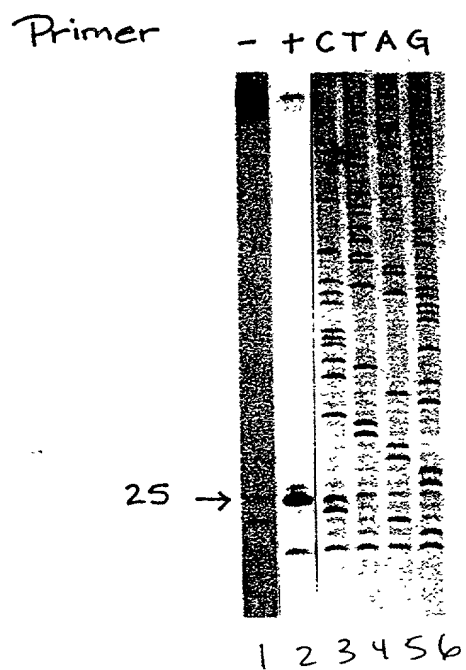


FIGURE 65



FIGURE 66

